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Copyright (c) 1993 - 2003 Compugen Ltd.	GenCore version 5.1.3				
Run on:	January 17, 2003, 19:18:18 ; Search time 15 Seconds (without alignments)				
Scoring table:	BLOSUM62				
Searched:	Gapext 0.5 262574 seqs., 29422922 residues				
Total number of hits satisfying chosen parameters:	262574				
Post-processing: Minimum Match 0%	Maximum Match 100%				
Database :	Listing first 45 summaries				
Result No.	Score	Query	Match Length	DB ID	Description
1	1441	100.0	271	2	US-08-467-265-2
2	1441	100.0	271	4	US-08-467-265-2
3	1441	100.0	271	4	US-09-407-891-2
4	740	51.4	198	2	US-08-467-265-15
5	740	51.4	198	4	US-08-467-265-15
6	721.5	50.1	199	2	US-08-467-265-17
7	721.5	50.1	199	4	US-08-467-265-17
8	721.5	50.1	199	4	US-08-467-265-17
9	721.5	50.1	199	4	US-09-407-891-17
10	713.5	49.5	199	1	US-08-219-162A-2
11	713.5	49.5	199	2	US-08-219-162A-2
12	713.5	49.5	199	4	US-08-467-265-14
13	713.5	49.5	199	4	US-08-407-891-14
14	689	47.8	257	2	US-08-467-265-16
15	689	47.8	257	4	US-08-467-265-16
16	689	47.8	257	4	US-09-407-891-16
17	683	47.4	199	1	US-08-602-262-2
18	683	47.4	199	3	US-09-004-716-2
19	619	43.0	178	1	US-08-219-162A-4
20	587	40.7	199	4	US-09-183-861-24
21	587	40.7	199	4	US-09-072-705-24
22	586	40.7	206	4	US-09-183-861-26
23	586	40.7	206	4	US-09-072-705-26
24	462	32.1	202	4	US-09-556-877-92
25	462	32.1	202	4	US-09-620-412C-92
26	457	31.7	195	4	US-09-556-877-65
27	31.7	4	US-09-620-412C-65		
QY	1	MEALPLLAATTDPDGRHRRLLLPLPLFLPAGAVGQWGVETEPRTREECHFYAGQVY	60		
Db	1	MEALPLLAATTDPDGRHRRLLLPLPLFLPAGAVGQWGVETEPRTREECHFYAGQVY	60		

QY 61 PGEASRVSVADHSLSKAKISKAPYWGCTAVIDGEFKEKLTDYRGKLVFFYPLDF 120
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 61 PGEASRVSVADHSLSKAKISKAPYWGCTAVIDGEFKEKLTDYRGKLVFFYPLDF 120
 QY 121 TFVCPTTEIAFGDRLEFRSINTEVACSVDSQFTHLAWINTPRRQGLGPIRPLSDL 180
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 121 TFVCPTTEIAFGDRLEFRSINTEVACSVDSQFTHLAWINTPRRQGLGPIRPLSDL 180
 QY 181 THQISKDGYYLEDSGHTLGLFTIDDKGLRQTLNDLPGVGRSDETLRLVQAFQYTK 240
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 181 THQISKDGYYLEDSGHTLGLFTIDDKGLRQTLNDLPGVGRSDETLRLVQAFQYTK 240
 QY 181 THQISKDGYYLEDSGHTLGLFTIDDKGLRQTLNDLPGVGRSDETLRLVQAFQYTK 240
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 181 THQISKDGYYLEDSGHTLGLFTIDDKGLRQTLNDLPGVGRSDETLRLVQAFQYTK 240
 QY 241 HGEVCPAGWKPGSETIIPDAGKLYFDKLN 271
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 241 HGEVCPAGWKPGSETIIPDAGKLYFDKLN 271
 RESULT 2
 US-08-467-265-2
 ; Sequence 2, Application US/08467265
 ; Patent No. 6255079
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; GENTZ, Reiner
 ; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ; STREET: 6 Becker Farm Road
 ; CITY: Roseland
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/467, 265
 ; FILING DATE: 06-Jun-1995
 ; CLASSIFICATION: <unknown>
 ATTORNEY/AGENT INFORMATION:
 ; NAME: Ferraro, Gregory D.
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 271 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 ; US-08-467-265-2
 Query Match 100.0%; Score 1441; DB 4; Length 271;
 Best Local Similarity 100.0%; Pred. No. 2.5e-157; Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MEALPLLAATTPDGHRRRLLLPPLFLPAGVQGVWETEERTRREBECHEFAGQVY 60
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 Db 1 MEALPLLAATTPDGHRRRLLLPPLFLPAGVQGVWETEERTRREBECHEFAGQVY 60
 QY 61 PGEASRVSVADHSLSKAKISKAPYWGCTAVIDGEFKEKLTDYRGKLVFFYPLDF 120
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 Db 61 PGEASRVSVADHSLSKAKISKAPYWGCTAVIDGEFKEKLTDYRGKLVFFYPLDF 120
 QY 61 PGEASRVSVADHSLSKAKISKAPYWGCTAVIDGEFKEKLTDYRGKLVFFYPLDF 120
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 Db 61 PGEASRVSVADHSLSKAKISKAPYWGCTAVIDGEFKEKLTDYRGKLVFFYPLDF 120
 QY 121 TFVCPTTEIAFGDRLEFRSINTEVACSVDSQFTHLAWINTPRRQGLGPIRPLSDL 180
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 Db 121 TFVCPTTEIAFGDRLEFRSINTEVACSVDSQFTHLAWINTPRRQGLGPIRPLSDL 180
 QY 181 THQISKDGYYLEDSGHTLGLFTIDDKGLRQTLNDLPGVGRSDETLRLVQAFQYTK 240
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 181 THQISKDGYYLEDSGHTLGLFTIDDKGLRQTLNDLPGVGRSDETLRLVQAFQYTK 240
 QY 241 HGEVCPAGWKPGSETIIPDAGKLYFDKLN 271
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 241 HGEVCPAGWKPGSETIIPDAGKLYFDKLN 271
 RESULT 3
 US-09-407-891-2
 ; Sequence 2, Application US/09407891
 ; Patent No. 6294114
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; GENTZ, Reiner
 ; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ; STREET: 6 Becker Farm Road
 ; CITY: Roseland
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/407, 891
 ; FILING DATE: 06-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 ; NAME: Ferraro, Gregory D.
 ; REGISTRATION NUMBER: 36,134
 ; REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 271 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-407-891-2
 Query Match 100.0%; Score 1441; DB 4; Length 271;
 Best Local Similarity 100.0%; Pred. No. 2.5e-157; Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4 US-08-467-265-15

; Sequence 15, Application US/08467265

Patent No. 5985612

GENERAL INFORMATION:

APPLICANT: Ni, Jian

APPLICANT: Yu, Guo-Liang

APPLICANT: Gentz, Reiner

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

ADDRESS: STUART & OLSTEIN

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,265

FILED DATE: 06-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ferraro, Gregory D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-456

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 198 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-08-467-265-15

Query Match 51.4%; Score 740; DB 4; Length 198;

Best Local Similarity 69.9%; Pred. No. 5.8e-77;

Matches 135; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

MOLECULE TYPE: protein

Query Match 51.4%; Score 740; DB 2; Length 198;

Best Local Similarity 69.9%; Pred. No. 5.8e-77;

Matches 135; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

Query 79 AKISKPAPWEGTAVIDGERKELKLTDYRGKLVFFYPLDFTFVCPTEITAFGDDLEEF 138

Db 6 ARIGKAPABDFKATAVDGAFKEYKLSDYKGKVWLFYPLDFTFVCPTEITAFSRAEDF 65

Query 79 AKISKPAPWEGTAVIDGERKELKLTDYRGKLVFFYPLDFTFVCPTEITAFGDDLEEF 138

Db 6 ARIGKAPABDFKATAVDGAFKEYKLSDYKGKVWLFYPLDFTFVCPTEITAFSRAEDF 65

Query 139 RSINTTEVVAQSVDQSFTHLAWINTPRQGGGLPIRPLSLTHOISKDGYVLEDSHT 198

Db 66 RKLGEVLGVSVDSQFHNLAWINTPRKEGGGLPNIPLGDVIRRLSDEGYVLTDEGIA 125

Query 199 LRGFLFDKGILRQTTNDLPGRSVDETURLVQAFOYDKHGEVCPAGWKPGSETIP 258

Db 6 ARIGKAPADPKATAVDGAFKEYKLSDYKGKVWLFYPLDFTFVCPTEITAFSRAEDF 65

Query 139 RSINTTEVVAQSVDQSFTHLAWINTPRQGGGLPIRPLSLTHOISKDGYVLEDSHT 198

Db 126 YRGFLFDKGVLQRTVNDLPGVRSVDEALRLVQAFOYDEHGEVCPAGWKPGSTDTPK 185

Query 259 DPAGKLYFKDLN 271

Db 186 NVDSSKEYFSKH 198

RESULT 5 US-08-467-265-15

; Sequence 15, Application US/08467265

Patent No. 6225079

GENERAL INFORMATION:

APPLICANT: Ni, Jian

APPLICANT: Yu, Guo-Liang

APPLICANT: Gentz, Reiner

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

ADDRESS: STUART & OLSTEIN

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,265

FILING DATE: 06-Jun-1995

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Ferraro, Gregory D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-456

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 198 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-08-467-265-15

Query Match 51.4%; Score 740; DB 4; Length 198;

Best Local Similarity 69.9%; Pred. No. 5.8e-77;

Matches 135; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

Query 79 AKISKPAPWEGTAVIDGERKELKLTDYRGKLVFFYPLDFTFVCPTEITAFGDDLEEF 138

Db 6 ARIGKAPABDFKATAVDGAFKEYKLSDYKGKVWLFYPLDFTFVCPTEITAFSRAEDF 65

Query 139 RSINTTEVVAQSVDQSFTHLAWINTPRQGGGLPIRPLSLTHOISKDGYVLEDSHT 198

Db 66 RKLGEVLGVSVDSQFHNLAWINTPRKEGGGLPNIPLGDVIRRLSDEGYVLTDEGIA 125

Query 199 LRGFLFDKGILRQTTNDLPGRSVDETURLVQAFOYDKHGEVCPAGWKPGSETIP 258

Db 6 ARIGKAPADPKATAVDGAFKEYKLSDYKGKVWLFYPLDFTFVCPTEITAFSRAEDF 65

Query 139 RSINTTEVVAQSVDQSFTHLAWINTPRQGGGLPIRPLSLTHOISKDGYVLEDSHT 198

Db 126 YRGFLFDKGVLQRTVNDLPGVRSVDEALRLVQAFOYDEHGEVCPAGWKPGSTDTPK 185

Query 259 DPAGKLYFKDLN 271

Db 186 NVDSSKEYFSKH 198

RESULT 6 US-09-407-891-15

; Sequence 15, Application US/09407891

STATE: New Jersey
 COUNTRY: USA
 ZIP: 07668
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 FILING DATE: 06-Jun-1995
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/467,265
 FILING DATE: 06-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 199 amino acids
 TYPE: amino acid
 STRANDEDNESS: <unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 US-08-467-265-17

 Query Match 50.1%; Score 721.5; DB 4; length 199;
 Best Local Similarity 68.8%; Pred. No. 7.8e-75;
 Matches 132; Conservative 27; Mismatches 32; Indels 1; Gaps 1;
 QY 79 AKISKPAPYWESTAVI-DGEFFKELKLTDYRGKLVFFPFYPLDFTVCPTEIAFGDRLEE 137
 Db 6 AKIGYPAPNFKATAVMPDGQFDISLSEYKGKVVFYPLDFTVCPTEIAFGDRLEE 65
 Db 66 FKKLNQCQVIGASVDHFCHLAWINTPKQGGGPMNPLISPDKRITAQDVKVLADEGI 125
 QY 138 FRSINTEVVACVSQDSQFTHLAWINTPRRGGLGPIRPLSLDTHQTSKDVGVYLEDSGH 197
 Db 66 FKKLNQCQVIGASVDHFCHLAWINTPKQGGGPMNPLISPDKRITAQDVKVLADEGI 125
 QY 198 TRLGLFLIDDKGILRQITLNDLPGVRSDETIRLVQFOYTQKHHGEVCAGWKPGSETII 257
 Db 126 SFRGLFIDDKGILRQITLNDLPGVRSDETIRLVQFOYTQKHHGEVCAGWKPGSETII 185
 QY 258 PPGAKLKYFDK 269
 Db 186 PDVNSKEYFSK 197

 RESULT 9
 US-09-07-891-17
 Sequence 17, Application US/09407891
 ; Patient No. 629164
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Gantz, Reiner
 ; APPLICANT: Rosen, Craig A.
 ; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNIE, BAIN, GILFILLAN, CECCHI,
 ; STREET: 6 Becker Farm Road
 ; CITY: Roseland
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/299,162A
 ; FILING DATE: August 31, 1994
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Oldenkamp, David J
 ; REFERENCE/DOCKET NUMBER: 104-280

QY 79 AKISKPAPWEGTAVI-DGEEFKELKLTDYRGKLYVFFYPLDFTCVCPBIAFGDRLEE 137
 Db 6 FKKLNQVIGASVDSFHCLAWNWPKQSGLGPNIPLVSDPKRITAQDGVLKADEGI 125
 Db 6 AKIGHAPAPNFKATAVMPDGFKDTSLSYKGKVYVFPLDFTCVCPTEILIAFSRAEE 65

QY 138 FRSTINTEVVACSVSDQSFTHAWINTPRROGGLGPIRIPPLSLDTHQSKDYGVILEDSGH 197
 Db 66 FKKLNQVIGASVDSFHCLAWNWPKQSGLGPNIPLVSDPKRITAQDGVLKADEGI 125
 Db 66 FKKLNQVIGASVDSFHCLAWNWPKQSGLGPNIPLVSDPKRITAQDGVLKADEGI 125

QY 198 TLRGFLFIDDKGILRQITLNDLPGRSVDETLRLVQAFOYTDKIGEVCPAGWKPGSETII 257
 Db 126 SFRGLFLIDDKGILRQITLNDLPGRSVDETLRLVQAFOYTDKIGEVCPAGWKPGSETII 185
 Db 126 SFRGLFLIDDKGILRQITLNDLPGRSVDETLRLVQAFOYTDKIGEVCPAGWKPGSETII 185

QY 258 PDPAGKLKYFDK 269
 Db 186 PDVPKTKEYFSK 197

RESULT 13
 US-09-407-891-14
 ; Sequence 14, Application US/09407891
 ; Patent No. 6294164
 ; GENERAL INFORMATION:
 ; APPLICANT: NI, Jian
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: GENTZ, Reiner
 ; APPLICANT: Rosen, Craig A.
 ; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
 ; NUMBER OF SEQUENCES: 17
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
 ; STREET: 6 Becker Farm Road
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, version #1.30

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/407,891
 FILING DATE: 2001-09-17
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferraro, Gregory D.
 REGISTRATION NUMBER: 36,134
 REFERENCE/DOCKET NUMBER: 325800-456
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-994-1700
 TELEFAX: 201-994-1744
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 199 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-407-891-14

Query Match 49.5%; Score 713.5; DB 4; Length 199;
 Best Local Similarity 68.8%; Pred. No. 6.5e-74;
 Matches 132; Conservative 25; Mismatches 34; Indels 1; Gaps 1;

QY 79 AKISKPAPWEGTAVI-DGEEFKELKLTDYRGKLYVFFYPLDFTCVCPBIAFGDRLEE 137
 Db 66 VTOHAPYFKGKPAVNGEKFSLSDPKGVLYPLDFTCVCPTEILIAFSRAEE 65

QY 141 INTEVVACSVSDQSFTHAWINTPRROGGLGPIRIPPLSLDTHQSKDYGVILEDSHTLR 200
 Db 126 VNCEVVAWSVDSFHCLAWNWPKQSGLGPNIPLVSDPKRITAQDGVLKADEGI 185
 Db 66 VTQHAPYFKGKPAVNGEKFSLSDPKGVLYPLDFTCVCPTEILIAFSRAEE 125

QY 201 GLFIDDKGILRQITLNDLPGRSVDETLRLVQAFOYTDKIGEVCPAGWKPGSETII 260
 Db 186 GLFIDDPNGVVKHLSVNDLPGVGRSVEETLRLVKAFOVFTGEVCPAGWKPGSETII 245

QY 261 AGKLKYFDKLN 271

Db 246 TASKEYFEKVH 256

RESULT 15

US-08-467-265-16

; Sequence 15, Application US/08467265

Patent No. 6255079

GENERAL INFORMATION:

APPLICANT: Ni, Jian

Yu, Guo-Liang

Rosen, Craig A.

Gentz, Reiner

Rosen, Craig A.

TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BATN, GILFILLAN, CECCHI,

STREET: 6 Becker Farm Road

CITY: Roseland

STATE: New Jersey

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/467,265

FILING DATE: 06-JUN-1995

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Ferraro, Gregory D.

REGISTRATION NUMBER: 36,134

REFERENCE DOCKET NUMBER: 325800-456

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

MOLECULE TYPE: protein

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-08-467-265-16

Query Match 47.8%; Score 689; DB 4; Length 257;

Best Local Similarity 64.4%; Pred. No. 6.3e-71; Mismatches 36; Indels 0; Gaps 0;

Matches 123; Conservative 32; Mismatches 36; Indels 0; Gaps 0;

Qy 81 ISKAPAYWEGTAVIDGERKELKLTDYRGKYLFFFYPLDFTFCPTETIAFGDRLEERS 140

Db 66 VTOHAPYFKGTAVNGEKFELSLDFKGKVLFFYPLDFTFCPTETIAFGDRLEERS 125

Qy 141 INPFWVAVSVDSOFTHLAWINPRQGLGPPIRIPULSDLTQISKOQYVYLEDSGITLR 200

Db 126 VNCEEVAVAVSVDSHFLAWINTPRKNGGLGHWNITLSDITKQISROYGVLESAGFLR 185

Qy 201 GUFIDDKGILROITLNDLPVGRSVDTELRLVQAFQVTDKHOEVCPAGWKPOSETTIPDP 260

Db 186 GSFIDPQVWHLSVNDLPVGRSVEETRLVKAQFVETGEVCPANWTPBSPTIKPSP 245

Qy 261 AGKLKYFDKLN 271

Db 246 TASKEYFEKVH 256

Search completed: January 17, 2003, 19:19:59
Job time : 17 secs

GenCore version 5.1.3
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Om protein - protein search, using SW model
 Run on: January 17, 2003, 19:18:27 ; Search time 13 Seconds
 (without alignments)
 414,391 Million cell updates/sec

Title: US-09-911-346-2
 Perfect score: 1441
 Sequence: 1 MEALPLLAATPDPDGHRRRL.....GSETTIPDPAGKLKYFDKLN 271

Scoring table: BL0SUM62
 Gapext 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database : Published Applications_AA,*
 1: /cgn2_6/ptodata/1/pubpea/US08_NEW_PUB.pep:/*
 2: /cgn2_6/ptodata/1/pubpea/PCT_NEW_PUB.pep:/*
 3: /cgn2_6/ptodata/1/pubpea/US06_PUBCOMB.pep:/*
 4: /cgn2_6/ptodata/1/pubpea/US07_NEW_PUB.pep:/*
 5: /cgn2_6/ptodata/1/pubpea/US07_PUBCOMB.pep:/*
 6: /cgn2_6/ptodata/1/pubpea/US07_PUBCOMB.pep:/*
 7: /cgn2_6/ptodata/1/pubpea/PC1US_PUBCOMB.pep:/*
 8: /cgn2_6/ptodata/1/pubpea/US08_PUBCOMB.pep:/*
 9: /cgn2_6/ptodata/1/pubpea/US09_NEW_PUB.pep:/*
 10: /cgn2_6/ptodata/1/pubpea/US09_PUBCOMB.pep:/*
 11: /cgn2_6/ptodata/1/pubpea/US10_NEW_PUB.pep:/*
 12: /cgn2_6/ptodata/1/pubpea/US10_PUBCOMB.pep:/*
 13: /cgn2_6/ptodata/1/pubpea/US60_NEW_PUB.pep:/*
 14: /cgn2_6/ptodata/1/pubpea/US60_PUBCOMB.pep:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1441	100.0	271	Sequence 2, Appl1
2	750.5	52.1	233	Sequence 973, App
3	740	51.4	198	Sequence 15, Appl
4	721.5	50.1	199	Sequence 17, Appl
5	713.5	49.9	100	Sequence 14, Appl
6	703	48.8	224	Sequence 1537, Appl
7	689	47.8	257	Sequence 16, Appl
8	598	41.5	926	Sequence 128, App
9	598	41.5	955	Sequence 127, App
10	598	41.5	982	Sequence 95, Appl
11	598	41.5	982	Sequence 95, Appl
12	598	41.5	1427	Sequence 97, Appl
13	598	41.5	1427	Sequence 97, Appl
14	598	41.5	1641	Sequence 96, Appl
15	598	41.5	1641	Sequence 96, Appl
16	591	41.0	446	Sequence 1121, App
17	591	41.0	446	Sequence 1121, App
18	591	41.0	1464	Sequence 1008, App
19	587	40.7	199	Sequence 24, Appl

ALIGNMENTS

RESULT	1
US-09-911-346-2	; Sequence 2, Application US/09911346
	; Patent No. US20020106523A1
	; GENERAL INFORMATION:
	APPLICANT: Ni, Jian
	Yu, Guo-Liang
	Gentz, Reiner
	Rosen, Craig A.
	TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
	NUMBER OF SEQUENCES: 17
	CORRESPONDENCE ADDRESS:
	ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
	STREET: 6 Becker Farm Road
	CITY: Roseland
	STATE: New Jersey
	COUNTRY: USA
	ZIP: 07068
	COMPUTER READABLE FORM:
	MEDIUM TYPE: Floppy disk
	COMPUTER: IBM PC compatible
	OPERATING SYSTEM: PC-DOS/MS-DOS
	SOFTWARE: PatentIn Release #1.0, Version #1.30
	CURRENT APPLICATION DATA:
	APPLICATION NUMBER: US/09/911,346
	FILING DATE: 24-Jul-2001
	CLASSIFICATION: <Unknown>
	PRIOR APPLICATION DATA:
	APPLICATION NUMBER: US 08/467,265
	FILING DATE: 06-Jun-1995
	ATTORNEY/AGENT INFORMATION:
	NAME: Ferraro, Gregory D.
	REGISTRATION NUMBER: 36,134
	REFERENCE/DOCKET NUMBER: 32500-456
	TELECOMMUNICATION INFORMATION:
	TELEPHONE: 201-994-1700
	TELEFAX: 201-994-1744
	INFORMATION FOR SEQ ID NO: 2:
	SEQUENCE CHARACTERISTICS:
	LENGTH: 271 amino acids
	TYPE: amino acid

; TOPOLGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-911-346-2

Query Match 100.0%; Score 1441; DB 10; Length 271;
Best Local Similarity 100.0%; Pred. No. 5.7e-139; Indels 0; Gaps 0;
Matches 271; Conservative 0; Mismatches 0; Incls 0; Gaps 0;

Qy 1 MEALPPLAATTPDGHRRRLPLLFLPAGAVQGVWETEERPTREFECHYAGQVY 60
Db 1 MEALPPLAATTPDGHRRRLPLLFLPAGAVQGVWETEERPTREFECHYAGQVY 60

Qy 61 PGEASRVSDAHSLSKAKISKAPYWGTAVIDGEFKEKLTDYGRKLVLFFFYPLDF 120
Db 61 PGEASRVSDAHSLSKAKISKAPYWGTAVIDGEFKEKLTDYGRKLVLFFFYPLDF 120

Qy 121 TFWCPTTEIAFGDRLEEFRSINTPVACSYSDFTPLAWINTPRQGLGPITPLSLD 180
Db 121 TFWCPTTEIAFGDRLEEFRSINTPVACSYSDFTPLAWINTPRQGLGPITPLSLD 180

Qy 181 THQISKDGYVYLDSGHTLRLGLRQITNDLPVGSVDETLRLVQAFOYIDK 240
Db 181 THQISKDGYVYLDSGHTLRLGLRQITNDLPVGSVDETLRLVQAFOYIDK 240

Qy 241 HGEVCVPAGWKPGSETIIPDPAGKLYFDKLN 271
Db 241 HGEVCVPAGWKPGSETIIPDPAGKLYFDKLN 271

RESULT 2

US-09-925-301-973

; Sequence 93, Application US/09925301

; Patient No. US20020522308A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: PA106

; CURRENT APPLICATION NUMBER: US/09/925, 301

; PRIORITY APPLICATION NUMBER: PCT/US00/05882

; PRIORITY FILING DATE: 2000-03-08

; PRIORITY FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 1694

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 973

; LENGTH: 233

; TYPE: PR

; ORGANISM: Homo sapiens

; FEATURE: SITE

; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

Query Match 52.1%; Score 750.5; DB 10; Length 233;
Best Local Similarity 67.1%; Pred. No. 7.9e-69; Indels 1; Gaps 1;

Matches 139; Conservative 27; Mismatches 40; Incls 1; Gaps 1;

Qy 64 ASRVSVDASHLSKAKISKAPYWGTAVIDGEFKEKLTDYGRKLVLFFFYPLDF 122

Db 25 ATCVGTAOKRNSGKAPYWGTAVIDGEFKEKLTDYGRKLVLFFFYPLDF 138

Qy 123 VCPTEIAFGDRLEERSINTEVACSVDSOFTLAWINTPRQGLGPTRIPLSLDTH 182

Db 85 VCPTEIAFGDRLEERSINTEVACSVDSOFTLAWINTPRQGLGPTRIPLSLDTH 182

Qy 183 QISKDGYVLEDGHTLRLGLPFTIDKGILRQITNDLPVGSRVDETLRLVQAFOYIDK 242

Db 145 TIAQDQVLRKADEGSFRGLFIIIDKGILRQITNDLPVGSRVDETLRLVQAFOYIDK 204

Qy 243 EVCPAGWKPGSETIIPDPAGKLYFDKLN 269

; TOPOLGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
; US-09-911-346-2

RESULT 3
; Sequence 15, Application US/09911346
; Patient No. US2002010623A1
; GENERAL INFORMATION:

; APPLICANT: Ni, Jian

; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRN, BAIN, GILFILLAN, CECCHI,

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/911,346

; FILING DATE: 24-Jul-2001

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/467,265

; ATTORNEY/AGENT INFORMATION:

; NAME: Ferraro, Gregory D.

; REGISTRATION NUMBER: 35,134

; REFERENCE/DOCKET NUMBER: 325800-456

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 198 amino acids

; TYPE: amino acid

; STRANEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 15:

; US-09-911-346-15

Query Match 51.4%; Score 740; DB 10; Length 198;
Best Local Similarity 69.9%; Pred. No. 7.3e-68; Indels 0; Gaps 0;
Matches 135; Conservative 25; Mismatches 33; Incls 0; Gaps 0;

Qy 79 AKISKDGYVLEDGHTLRLGLPFTIDKGILRQITNDLPVGSRVDETLRLVQAFOYIDK 198

Db 6 ARIGKAPDPDKATAVDPGKDFKDISLSDYKQVVFYPLDFTE 65

Qy 139 RSINTEVACSVDSOFTLAWINTPRQGLGPTRIPLSLDTHQISKDGYVLDGHT 198

Db 66 RKLGEVLGYSVDSQFNHLAWINTPRQGLGPTRIPLSLDTHQISKDGYVLDGHT 125

Qy 199 LRGLFIDDDGILRQITNDLPVGSRVDETLRLVQAFOYIDKHEGVCPAGWKPGSETIIP 258

Db 126 YRGLEFIDDGKVLRQITNDLPVGSRVDETLRLVQAFOYIDKHEGVCPAGWKPGSETIIP 185

Qy 259 DPAGKLYFDKLN 271

Db 186 NVDSKEYFSKH 198

RESULT 4
US-09-911-346-17
; Sequence 17, Application US/09911346
; Patent No. US2002016323A1
GENERAL INFORMATION:
APPLICANT: Ni, Jian
YU, Guo-Liang
Gentz, Reiner
Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/911,346
FILING DATE: 24-JUL-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,265
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Farraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLogy: Linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-911-346-17
Query Match 50.1% Score 721.5; DB 10; Length 199;
Best Local Similarity 68.8%; Pred. No. 5.6e-65;
Matches 132; Conservative 27; Mismatches 32; Indels 1; Gaps 1;
Query 79 AKTSKPAWEGTAVI-DGEFEKLKDYRGKLVNPFYPPLDFTFWCPTEITAFGDRLEE 137
Db 6 AKIGYPPAPNFKAATVMPDGQFDISLSEYKGKVWFFYPLPFTFWCPTEITAFSRAEE 65
Query 138 FRSTNTENVACSYDSQFTHLAWINTPRROGGLGPIRLPLSDLTHOITSKYDGYVLERSGH 197
Db 66 FKKLNCOVIGASVDSHFCHLAWNPTRPKQGGLGPMNIPLSDPKRTIAQDYGVLKADEGI 125
Query 198 TRLGLFIDDKGILRQITLNDLPGRSVDETLRQLVAQFQYTKHGEVCAGWKPGSETII 257
: |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||
Db 126 SFRGLFIDDKGILRQITVNDPCCRSVDETLRQLVAQFQFTDKHGEVCAGWKPGSDTIK 185
Query 258 PDPAGKLKFDFK 269
: |||
Db 186 PDVKPKTFYFSK 197
RESULT 6
US-09-925-300-1537
; Sequence 1537, Application US/09925300
; Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
; Applicant: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

RESULT 5
US-09-911-346-14
; Sequence 14, Application US/09911346
; Patent No. US2002016323A1

; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIORITY APPLICATION NUMBER: PCT/US00/05988
; PRIORITY FILING DATE: 2000-03-08
; PRIORITY APPLICATION NUMBER: 60/124,270
; PRIORITY FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 1537
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-925,300-1537
; Query Match 48.8%; Score 703; DB 10; Length 224;
; Best Local Similarity 66.5%; Pred. No. Se-64;
; Matches 127; Conservative 28; Mismatches 36; Indels 0; Gaps 0;
; Qy 81 ISKAPAPIWEGTAVIDGEFKALKLTYRKGKLVFFFYPLDFTVCPETEIAGDRLEEFRS 140
; Db 33 VTQHAPYFKGTAVNGEKFQKLSDFDKGKVLVLFYPLDFTVCPETEIVAFSDKANEFH 92
; Qy 141 INTEVACVSQDSOFTHLAWNTPRROGGIGPIRIPSLSDTHOISKDYGYLEDSGHTLR 200
; Db 93 VNCCEVAVASVDHSFLHAWNTPRNGGLGHMNLISDJKTQISRDYGVWILEGSSLALR 152
; Qy 201 GLFIIDDKGILRQITLNDLPGVSDETLRVQAFQYTDKHGEVCPAGWKPGSETIIPDP 260
; Db 153 GLFIDDPNGVKHLSVNDLPGVRSVEETRLVKAFOVYTHEGEVCPANWTPDSTIKPSP 212
; Qy 261 AGKKYFDKLN 271
; Db 213 AASKEYFOKVN 223
; RESULT 7
; Sequence 16, Application US/09911346
; Patent No. US20020106523A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; YU, Guo-Jiang
; Genitz, Reiner
; Rosent, Craig A.
; TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARILLA, BYRNE, BAIN, GILLILLAN, CECCHI,
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/911,346
; FILING DATE: 24-JUL-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,265
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-456
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-94-1700
; US-09-911-346-16
; Query Match 47.8%; Score 689; DB 10; Length 257;
; Best Local Similarity 64.4%; Pred. No. 1.6e-62;
; Matches 123; Conservative 32; Mismatches 36; Indels 0; Gaps 0;
; Qy 81 ISKAPAPIWEGTAVIDGEFKALKLTYRKGKLVFFFYPLDFTVCPETEIAGDRLEEFRS 140
; Db 66 VTQHAPYFKGTAVNGEKFQKLSDFDKGKVLVLFYPLDFTVCPETEIVAFSDKANEFH 125
; Qy 141 INTEVACVSQDSOFTHLAWNTPRROGGIGPIRIPSLSDTHOISKDYGYLEDSGHTLR 200
; Db 126 VNCCEVAVASVDHSFLHAWNTPRNGGLGHMNLISDJKTQISRDYGVLESAGTLR 185
; Qy 201 GLFIIDDKGILRQITLNDLPGVSDETLRVQAFQYTDKHGEVCPAGWKPGSETIIPDP 260
; Db 186 GLFIDDPNGVKHLSVNDLPGVRSVEETRLVKAFOVYTHEGEVCPANWTPDSTIKPSP 245
; Qy 261 AGKKYFDKLN 271
; Db 246 TASKEYFEKVH 256
; RESULT 8
; Sequence 128, Application US/09991496
; Patent No. US200201069285A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bratia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; APPLICANT: Brannon, Mark
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121_420C9
; CURRENT APPLICATION NUMBER: US/09/991,496
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 926
; TYPE: PRT
; ORGANISM: Leishmania major
; US-09-991-496-128
; Query Match 41.5%; Score 598; DB 9; Length 926;
; Best Local Similarity 54.0%; Pred. No. 1.7e-52;
; Matches 108; Conservative 39; Mismatches 51; Indels 2; Gaps 2;
; Qy 72 HSLHLASKAKISKAPYMEGTAVI-DGERKELKLTDRKGKLYVFFFYPLDFTVCPETEIA 130
; Db 6 HIMSCKGNAKINSAPSFEVALMPNGSFKKISLSSYKGKWWVLLFFYPLDFTVCPETEIA 65
; Qy 131 FGDRLLEFRSINTEVACVSQDSOFTHLAWNTPRROGGIGPIRIPSLSDTHOISKDGV 190
; Db 66 FSDSVARFENELCIVACISIDESSEYAHLOWLTDORKGSLGTMAIPLADTKTSIARSVG 125
; Qy 191 YLEDSGHTLRGLFIIDDKGILRQITLNDLPGVRSVDETLRVQAFQYTDKHGEVCPAGWK 250

Db 66 FSPSVSRFNELNCEVLAQCSIDSSEYAHQLWTLDRKKGGLGTMAIMPLADKTSIARSYGV 125 ; APPLICANT: Coler, Rhea
 Qy 191 YLEDSGHTLRLGFLIDDDKGILRQITLNDLPGRSVDETLRLVQAFOYTDKHGEVCAGWK 250 ; APPLICANT: Probst, Peter
 Db 126 LEESQGVAYRGFLIDPHGMQLRQITVNDMPVGRSVEEVRLLEAFQFVERKHGEVC PANWK 185 ; GENERAL INFORMATION:
 ; APPLICANT: Brannon, Mark
 ; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
 ; FILE REFERENCE: 210121.420C8
 ; CURRENT APPLICATION NUMBER: US/09/874, 923
 ; CURRENT FILING DATE: 2001-06-04
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 97
 ; LENGTH: 1427
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
 ; OTHER INFORMATION: Leishmania antigens

Query Match 41.5%; Score 598; DB 9; Length 1427;
 Best Local Similarity 54.0%; Pred. No. 3. 1e-52; Matches 108; Conservative 39; Mismatches 51; Indels 2; Gaps 2;

Qy 72 HSLHLSKAKISKPAPWEGAVI-DGEEFKELKLTDYRGKVLYFFFPLDIFVCPEVIA 130 ; APPLICANT: Campos-Neto, Antonio
 Db 6 HMSCGNAKINSPPAPSFEEVALMPNGFSKIKSSLSSYKGKWNVLFFYPLDIFVCPEVIA 65 ; APPLICANT: Webb, John R.
 Qy 131 FGDRLEFRSNTTEVACVSUSOFTHLAWIMPRROGGLGTRIPSLDLTHQSKDYGV 190 ; APPLICANT: Dillon, Devin C.
 Db 66 FSDSVSRFNELNCEVLAQCSIDSSEYAHQLWTLDRKKGGLGTMAIMPLADKTSIARSYGV 125 ; APPLICANT: Skeiky, Yasir A.W.
 Qy 191 YLEDSGHTLRLGFLIDDDKGILRQITLNDLPGRSVDETLRLVQAFOYTDKHGEVCAGWK 250 ; APPLICANT: Coler, Rhea
 Db 126 LEESQGVAYRGFLIDPHGMQLRQITVNDMPVGRSVEEVRLLEAFQFVERKHGEVC PANWK 185 ; APPLICANT: Probst, Peter
 Qy 251 PGSETIPDAGKL-YFDK 269 ; APPLICANT: Brannon, Mark
 Db 186 KGAPTMKPEPNASVEGYFSK 205 ; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
 ; FILE REFERENCE: 210121.420C9
 ; CURRENT APPLICATION NUMBER: US/09/991, 496
 ; CURRENT FILING DATE: 2001-11-20
 ; NUMBER OF SEQ ID NOS: 137
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 97
 ; LENGTH: 1427
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
 ; OTHER INFORMATION: Leishmania antigens

Query Match 41.5%; Score 598; DB 9; Length 1427;
 Best Local Similarity 54.0%; Pred. No. 3. 1e-52; Matches 108; Conservative 39; Mismatches 51; Indels 2; Gaps 2;

Qy 72 HSLHLSKAKISKPAPWEGAVI-DGEEFKELKLTDYRGKVLYFFFPLDIFVCPEVIA 130 ; APPLICANT: Campos-Neto, Antonio
 Db 6 HMSCGNAKINSPPAPSFEEVALMPNGFSKIKSSLSSYKGKWNVLFFYPLDIFVCPEVIA 65 ; APPLICANT: Webb, John R.
 Qy 131 FGDRLEFRSNTTEVACVSUSOFTHLAWIMPRROGGLGTRIPSLDLTHQSKDYGV 190 ; APPLICANT: Dillon, Devin C.
 Db 66 FSDSVSRFNELNCEVLAQCSIDSSEYAHQLWTLDRKKGGLGTMAIMPLADKTSIARSYGV 125 ; APPLICANT: Skeiky, Yasir A.W.
 Qy 191 YLEDSGHTLRLGFLIDDDKGILRQITLNDLPGRSVDETLRLVQAFOYTDKHGEVCAGWK 250 ; APPLICANT: Coler, Rhea
 Db 126 LEESQGVAYRGFLIDPHGMQLRQITVNDMPVGRSVEEVRLLEAFQFVERKHGEVC PANWK 185 ; APPLICANT: Probst, Peter
 Qy 251 PGSETIPDAGKL-YFDK 269 ; APPLICANT: Brannon, Mark
 Db 186 KGAPTMKPEPNASVEGYFSK 205 ; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
 ; FILE REFERENCE: 210121.420C9
 ; CURRENT APPLICATION NUMBER: US/09/991, 496
 ; CURRENT FILING DATE: 2001-11-20
 ; NUMBER OF SEQ ID NOS: 137
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 96
 ; LENGTH: 1641
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
 ; OTHER INFORMATION: Leishmania antigens

Query Match 41.5%; Score 598; DB 9; Length 1641;
 Best Local Similarity 54.0%; Pred. No. 3. 8e-52; Matches 108; Conservative 39; Mismatches 51; Indels 2; Gaps 2;

Qy 191 YLEDSGHTLRLGFLIDDDKGILRQITLNDLPGRSVDETLRLVQAFOYTDKHGEVCAGWK 250 ; APPLICANT: Coler, Rhea
 Db 126 LEESQGVAYRGFLIDPHGMQLRQITVNDMPVGRSVEEVRLLEAFQFVERKHGEVC PANWK 185 ; APPLICANT: Probst, Peter
 Qy 251 PGSETIPDAGKL-YFDK 269 ; APPLICANT: Brannon, Mark
 Db 186 KGAPTMKPEPNASVEGYFSK 205 ; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
 ; FILE REFERENCE: 210121.420C9
 ; CURRENT APPLICATION NUMBER: US/09/991, 496
 ; CURRENT FILING DATE: 2001-11-20
 ; NUMBER OF SEQ ID NOS: 137
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 96
 ; LENGTH: 1641
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
 ; OTHER INFORMATION: Leishmania antigens

Query Match 41.5%; Score 598; DB 9; Length 1641;
 Best Local Similarity 54.0%; Pred. No. 3. 8e-52; Matches 108; Conservative 39; Mismatches 51; Indels 2; Gaps 2;

QY 72 HSLHLISAKTISKPKDYGEGKELKLTDYRGKYLVFFYPLODTEVCPTETIA 130
 | : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 6 HHSMSGNAKINSPPSFEEVALMPNGSFKKLSSTYKGKAWVLFYPLDFTVCPTETIA 65
 QY 131 FGDRLEEFKISINTEVACSVSDQFHLMWINTPROGGIIPRIPLLSDLTHQSKDGY 190
 | : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 66 FSDSVSRFNLNECEVLACSIDSEYAHLOWTLDKRGKGTMAPMLADKTKSARSYGV 125
 QY 191 YLEDSGHTLRGLFLIDDKGILRQITLNDLVPGRSDETLRLVQAFOYTDKHGEVCPAGWK 250
 | : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 126 LEESQGVAYVGELIDPHGMURQTYNDMVGYSVEEVRLAEOFVEKHGEVCPANW 185
 QY 251 PGSETTIPDPAGKLK-YFDK 269
 | : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 186 KGAPIMKPEPNASVEGYFSK 205

RESULT 15
 US-09-874-923-96
 Sequence 96, Application US/09874923
 Patent No. US20020081320A1
 GENERAL INFORMATION:
 APPLICANT: Reed, Steven G.
 APPLICANT: Campos Neto, Antonio
 APPLICANT: Webb, John R.
 APPLICANT: Dillon, Davin C.
 APPLICANT: Skeiky, Yasir A.W.
 APPLICANT: Bhatia, Ajay
 APPLICANT: Coler, Rhea
 APPLICANT: Probst, Peter
 APPLICANT: Brannon, Mark
 TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
 THERAPY AND DIAGNOSIS OF LEISHMANIASIS
 FILE REFERENCE: 210121_420CB
 CURRENT APPLICATION NUMBER: US/09/874, 923
 CURRENT FILING DATE: 2001-06-04
 NUMBER OF SEQ ID NOS: 122
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 96
 LENGTH: 1641
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Fusion (poly-protein) constructs comprising multiple
 US-09-874-923-96

Query Match 41.5%; Score 598; DB 10; Length 1641;
 Best Local Similarity 54.0%; Pred. No. 3. 8e-52; Gaps 2;
 Matches 108; Conservative 39; Mismatches 51; Indels 2;

QY 72 HSLHLISAKTISKPKDYGEGKELKLTDYRGKYLVFFYPLODTEVCPTETIA 130
 | : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 6 HHSMSGNAKINSPPSFEEVALMPNGSFKKLSSTYKGKAWVLFYPLDFTVCPTETIA 65
 QY 131 FGDRLEEFKISINTEVACSVSDQFHLMWINTPROGGIIPRIPLLSDLTHQSKDGY 190
 | : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 66 FSDSVSRFNLNECEVLACSIDSEYAHLOWTLDKRGKGTMAPMLADKTKSARSYGV 125
 QY 191 YLEDSGHTLRGLFLIDDKGILRQITLNDLVPGRSDETLRLVQAFOYTDKHGEVCPAGWK 250
 | : ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 126 LEESQGVAYVGELIDPHGMURQTYNDMVGYSVEEVRLAEOFVEKHGEVCPANW 185
 QY 251 PGSETTIPDPAGKLK-YFDK 269
 | : ||| :||| :||| :||| :||| :||| :||| :||| :|||
 Db 186 KGAPIMKPEPNASVEGYFSK 205

Search completed: January 17, 2003, 19:20:23

Job time : 18 secs

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Gencore version 5.1.3

Run on:

January 17, 2003, 19:17:48 ; Search time 19 Seconds
(without alignments)
1371.180 Million cell updates/sec

Title: US-09-911-346-2

Perfect score: 1441

Sequence: 1 MEALPLLAATTPDHGRHRRL... GSETIIPDPAGKLKYFDKLN 271

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : Listing first 45 summaries

PIR_73;*

1: p11;*

2: p12;*

3: p13;*

4: p14;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
RESULT 1				
1	1441	100.0	271	2 G01790
2	744	51.6	198	2 A57716
3	740	51.4	198	2 168897
4	735.5	51.0	199	2 A46711
5	731.5	50.8	200	2 151016
6	730.5	50.7	199	2 152425
7	721.5	50.1	199	2 A48513
8	701	48.6	576	2 T16005
9	689	47.8	257	2 JQ0064
10	680	47.2	195	2 JC2258
11	639.5	44.4	226	2 S43598
12	634	44.0	192	2 T41413
13	588	40.8	203	2 A12385
14	588.5	40.8	210	2 T05318
15	584	40.5	196	2 A47362
16	582	40.4	265	2 T09211
17	570.5	39.6	200	2 S76284
18	568.5	39.5	242	2 S49173
19	567	39.5	196	2 S69732
20	548	38.0	199	2 S73193
21	479.5	33.3	233	2 S67947
22	477	33.1	178	2 S29119
23	477	33.1	200	2 A71689
24	474.5	32.9	199	2 F83540
25	474.5	32.9	273	2 A43862
26	467	32.4	202	2 C97756
27	461	32.0	200	2 G83204
28	455	31.6	195	2 G71492
29	451.5	31.3	200	2 AB0552

ALIGNMENTS

QY 1 MEALPLLAATTPDHGRHRRLPLPLFLPAGAVQWETEERPRTRFECHYAGGOW 60
Db 1 MEALPLLAATTPDHGRHRRLPLPLFLPAGAVQWETEERPRTRFECHYAGGOW 60
QY 61 PGEASRVSDHSUHLSKAKISKAPKAYPGWGTAVIDGERKEKLTDYRGKYLFFYPLDF 120
Db 61 PGEASRVSDHSUHLSKAKISKAPKAYPGWGTAVIDGERKEKLTDYRGKYLFFYPLDF 120
QY 121 TFCVCPTEITAFGDRLLEFFSINTEVACSVDSOFTHLAWINTPRQGGIGPIRPLSDL 180
Db 121 TFCVCPTEITAFGDRLLEFFSINTEVACSVDSOFTHLAWINTPRQGGIGPIRPLSDL 180
QY 181 THQISKDQYVYLESGHTTGLFLIDDKGILROITLNDLPGVGSVDETLVQAFQYD 240
Db 181 THQISKDQYVYLESGHTTGLFLIDDKGILROITLNDLPGVGSVDETLVQAFQYD 240
QY 241 HGEVCPAGWKPGSETIIPDPAGKLKYFDKLN 271
Db 241 HGEVCPAGWKPGSETIIPDPAGKLKYFDKLN 271

C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 11-Jun-1999
C;Accession: A57716
R;Chae, H.Z.; Robison, K.; Poole, L.B.; Church, G.; Storz, G.; Rhee, S.G.
Proc. Natl. Acad. Sci. U.S.A. 91, 7017-7021, 1994

A;Title: Cloning and Sequencing of thiol-specific antioxidant from mammalian brain: alkyl hydroperoxide reductase, C15-156/Domain: alkyl hydroperoxidase c22 protein
A;Reference number: A57716; MUID:94316629; PMID:8041738
A;Accession: A57716
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-198 <CHA>
C;Cross-references: GB:J06099; PID:9514253; PID:AAA19959_1; PID:9514254
C;Superfamily: alkyl hydroperoxide reductase c22 protein homology <C22>
F;15-156/Domain: alkyl hydroperoxidase c22 prot
Query Match Similarity 51.6%; Score 744; DB 2; Length 198;
Best Local Similarity 71.0%; Pred. No. 7.8e-61;
Matches 137; Conservative 22; Mismatches 34; Indels 0; Gaps 0;

Qy 79 AKISKPAPYWEQTAVIDGSEFKELKLTDYRGKLYVFFYPLDFTFVCPTEIAFGRLLEF 138
Db 6 AHICKPAPDPDTGTAWVGDAGFKEIKLSDRGRKVYLFLFPDFTFVCPTEIAFSRDAE 65
Qy 139 RSINTEVVACSVQSSQFTLHAWIINPRGGGLGPNILPILADYKMSLSONYGVLKNDGIA 198
Db 66 RKLGCCEVGLGVSYVSQFTLHAWIINPRGGGLGPNILPILADYKMSLSONYGVLKNDGIA 125
Qy 199 LRGIFLIDDKGILRQITNLDPVGSRVDETLRVQAFOYTDKHGEVCPAGWKPGSETIP 258
Db 126 YRGCFIIDKGIVRQITNLDPVGSRVDEALRLVQAFOYTDEHGEVCPAGWKPGSDTIKP 185
Qy 259 DPAGKLKYFDKLN 271
Db 186 NVDDSKEYFSKH 198

RESULT 3
18897 probable thioredoxin peroxidase (EC 1.11.1.-) 1 - human
M;Alternate names: enhancer protein; heme-binding 23k protein (HBP23); natural killer ce
C;Species: Homo sapiens (man)
C;Accession: I68897; I38341
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 02-Jun-2000
R;Shau, H.; Butterfield, L.H.; Chiu, R.; Kim, A.
Immunogenetics 40, 129-134, 1994
A;Title: Cloning and sequence analysis of candidate human natural killer-enhancing facto
A;Reference number: I54533; MUID:94299283; PMID:8026862
A;Accession: I68897
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: mRNA
A;Residues: 1-198 <SHA>
A;Cross-references: GB:LI19185; NID:9440307; PIDN:AAA50465.1; PID:9440308
R;Lim, Y.S.; Cha, M.K.; Kim, H.K.; Kim, I.H.
Gene 140, 279-284, 1994
A;Title: The thiol-specific antioxidant protein from human brain: gene cloning and analy
A;Reference number: I38341; MUID:94193012; PMID:8144038
A;Accession: I38341
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-158 <TVERTA'S'>,67-81,'T',83-104, 'A',106-119, 'N',121-174, 'R',176-179, 'R',181
A;Cross-references: EMBL:222548; NID:9438068; PID:CAA80269.; PID:9438069; GB:Li4286
A;Note: this sequence has been revised in EMBL:222548 and differs at positions 60-66 frd
C;Genetics:
A;Gene: GDB:TPX1; PRP; NKEFB
A;Cross-references: GDB:594943
A;Map position: 13q11-13q12
C;Superfamily: alkyl hydroperoxide reductase c22 protein; alkyl hydroperoxidase c22 prot
C;Keywords: heme; oxidoreductase
F;15-156/Domain: alkyl hydroperoxidase c22 protein homology <C22>
Query Match Similarity 51.0%; Score 735.5; DB 2; Length 199;
Best Local Similarity 70.3%; Pred. No. 4.7e-60;
Matches 135; Conservative 25; Mismatches 31; Indels 1; Gaps 1;

Qy 79 AKISKPAPYWEQTAVIDGSEFKELKLTDYRGKLYVFFYPLDFTFVCPTEIAFGRLLEF 137
Db 6 AKIKHPAPDPDTGTAWVGDAGFKEIKLSDRGRKVYLFLFPDFTFVCPTEIAFSRDAE 65
Qy 138 RSINTEVVACSVQSSQFTLHAWIINPRGGGLGPNILPILADYKMSLSONYGVLKNDGIA 197
Db 66 FKKLNCOVIGASVDSHFCHLAWNTPKQGGPMNIPLVSDPKRTIAQDYGVLKADEGI 125
Qy 198 TURGLFIDDKGILRQITNLDPVGSRVDEALRLVQAFOYTDEHGEVCPAGWKPGSETIP 257
Db 126 SFRLGLFIDDKGILRQITNLDPVGSRVDEALRLVQAFOYTDEHGEVCPAGWKPGSDTIKP 185
Qy 258 PDAGKLKYFDK 269
Db 186 PDVQSKYFSK 197

Query Match Similarity 51.4%; Score 740; DB 2; Length 198;
Best Local Similarity 69.9%; Pred. No. 1.8e-60;
Matches 135; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

Qy 79 AKISKPAPYWEQTAVIDGSEFKELKLTDYRGKLYVFFYPLDFTFVCPTEIAFGRLLEF 138
Db 6 ARIGKPAFPDKATAWVGDAGFKEVKSDYKGVVVFYPLDFTFVCPTEIAFSRDAE 65

RESULT 5
151016 proliferation associated protein pag homolog, 25k - Japanese common newt
C;Species: Cynops pyrhogaster (Japanese common newt)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 19-May-2000

C:Genetics:
A:Gene: CESP-F09E5.2
A;Introns: 54/1; 232/1; 281/3; 381/3; 507/1

Query Match 48.6%; Score 701; DB 2; Length 576;
Best Local Similarity 67.5%; Pred. No. 2, 8e-56;
Matches 131; Conservative 23; Mismatches 40; Indels 0; Gaps 0;

QY 76 LSKAKISKAPWEGTAVIDGERKEKLTDYRGKYLVFFFYPLDFTVCPTELIAFGDRL 135
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 382 MSRAFIGRAPAPQEQTKAQVDGEVDVSLSDYKGKKVYLFYPLDFTRVCPTELIAFGDRL 441
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 136 EERRSINTEVVACSVDSOFTHLAWINTPRROGLGPIRIPUSLTDHQISKDYGVYLED 195
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 442 EEFRAINTFVLAAMTSDSVFSHLAWINGOPRKHGGLEMNPVIAFDTNHQISRDYGVILKED 501
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 196 GHRLGLETIDDKGLRQITLNDLPGRSVDETLRLVQAFQYDQYDQYDQYDQYDQYDQYD 255
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 502 GIARGLFLTIDPSQNLROTIDNLPVGRSVDETLRLVQAFQYDQYDQYDQYDQYDQYDQ 561
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 256 IIPPDAGKLKYFDK 269
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 562 IKRGVKESQEYFKK 575

RESULT 9

JQ0064 MERS5 protein - mouse

C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jun-1999

C:Accession: JQ0064
R:Yamamoto, T.; Matsui, Y.; Natori, S.; Obinata, M.
Gene 80, 337-343, 1989
A:Title: Cloning of a housekeeping-type gene (MERS5) preferentially expressed in murine erythroid cells
A:Reference number: JQ0064; MUID:90060782; PMID:2563515

A:Accession: JQ0064
A:Molecule type: mRNA
A:Residues: 1-257 <YAM>
A:Cross-references: GB:M28723; NID:9309435; PIDN:AAA39524.1; PID:9309436
A:Note: the authors translated the codon GCT for residue 14 as Arg and CGT for 15 as Ala
C:Gene: MERS5
C:Superfamily: alkyl hydroperoxide reductase c22 protein; alkyl hydroperoxidase c22 protein
C:Keywords: mitochondrion
C:Domain: alkyl hydroperoxidase c22 protein homology <c22>

Query Match 47.8%; Score 689; DB 2; Length 257;
Best Local Similarity 64.4%; Pred. No. 1, 2e-55; Mismatches 36; Indels 0; Gaps 0;

QY 81 ISKPAPWEGTAVIDGERKEKLTDYRGKYLVFFFYPLDFTVCPTELIAFGDRL 123
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 124 GLFIIDPGVNGVKILSVNDLPGRSVEETLRLVKAFOQYEVAGCVPANWTPESPTIKPH 183
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 141 INTEVVACSVDSOFTHLAWINTPRROGLGPIRIPUSLTDHQISKDYGVYLEDGHTLR 200
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 64 VNCEVAVASVDHSFHSLAWINTPRKNGHNTIALSDETLHQISKDYGVYLEDGHLAR 123
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 201 GLFTIDDKGILRQITLNDLPGRSVDETLRLVQAFQYDQYDQYDQYDQYDQYDQYD 260
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 124 GLFIIDPGVNGVKILSVNDLPGRSVEETLRLVKAFOQYEVAGCVPANWTPESPTIKPH 183
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 261 AGRKLKYFDK 271
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 184 TASREYFEKVN 194

RESULT 11

S43598 mers5 homolog R07E5.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Accession: S43598
R:Innscoough, R.
submitted to the EMBL Data Library, April 1994
A:Reference number: S43595
A:Accession: S43598
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-226 <AIN>
A:Cross-references: EMBL:Z32683; NID:9474805; PID:9474809
A:Genetics:
A;Introns: 53/3; 197/3

C:Superfamily: alkyl hydroperoxide reductase c22 protein homology <c22>
F:42-183/Domain: alkyl hydroperoxidase c22 protein homology <c22>

Query Match 44.4%; Score 639.5; DB 2; Length 226;
Best Local Similarity 57.3%; Pred. No. 3, 7e-51; Mismatches 33; Indels 7; Gaps 1;

QY 141 INTEVVACSVDSOFTHLAWINTPRROGLGPIRIPUSLTDHQISKDYGVYLEDGHTLR 200
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 126 VNCEEVAVASVDHSFHSLAWINTPRKNGHNTIALSDETLHQISKDYGVYLEDGHLAR 185
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 201 GLFIIDDGKILRQITLNDLPGRSVDETLRLVQAFQYDQYDQYDQYDQYDQYDQYD 260
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 186 GLFIIDPGVNGVKILSVNDLPGRSVEETLRLVKAFOQYEVAGCVPANWTPESPTIKPH 245
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 261 AGKLKYFDKLN 271
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 246 TASREYFEKVN 256

QY 181 THQISKDYGVYLEDGHTLRGLFIDPGKILRQITLNDLPGRSVDETLRLVQAFQYDQYD 240
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 135 NKKIADSPGVLDKESGLSYRGLFLIDESGTVRHTCNDLPGRSVDETLRLVKAFOQYD 194
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 241 HGEVCPAGWKPKSESETIIPDPACKLYFDKLN 271
:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 195 HGEVCPADWHDSPTIKPGVATKEYFNKV 225

RESULT 10

JC2258 substrate protein of mitochondrial ATP-dependent proteinase SP-22 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999

RESULT 12
T41413 thioreddoxin peroxidase - fission yeast (Schizosaccharomyces pombe)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 20-Jun-2000
C;Accession: T41413; 150461
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z22954
A;Accession: T41413
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-192 <WOO>
A;Cross-references: EMBL:AL031798; PIDN:CAA21182.1; GSPDB:GN00068; SPDB:SPCC576.03C
A;Experimental source: strain 975h(-); cosmid c576
R;Koo, K.H.; Kim, K.; Chae, H.Z.
submitted to the EMBL Data Library, August 1998
A;Description: Thioreddoxin peroxidase from Schizosaccharomyces pombe.
A;Reference number: Z22073
A;Accession: T50461
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-192 <K002>
A;Cross-references: EMBL:AF083335; PIDN:AAC71013.1
C;Genetics:
A;Gene: SPDB-SPC576.03C
A;Map position: 3
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein
Query Match 44.0%; Score 634; DB 2; Length 192;
Best Local Similarity 60.0%; Pred. No. 9.6e-51; Matches 114; Conservative 36; Mismatches 38; Indels 2; Gaps 1;
Db 80 KISRPAPWEGTAVIDGEFKEKLTDYRGKYLFFFYPLDFTCPTILIAECDLERF 139
Qy 4 QICKPAPDFEKGTAVNGAFAEIKLADYKGKWWFLGFPFLDFTCPTIELVSEASRFA 63
Db 140 SINTEVVACSVSQQFTHAWINPPRQGLPPIRIPULSDLTHQISKDYGWLEDSGHL 199
Qy 64 ERNAQVILSTPSDESYHIAFNPTRKPGGGNIPNLADPSKIVSKVRSRDYGVLESAVF 123
Db 200 RGFLFIIDDKGILQITLNDLPLVGRSVDETLRLVQAFQYTDKIGEVCPAGWKPGSETIIPD 259
Qy 124 RGFLFIDPKGVLRQITINDLPVGRSVDEALRLDAQFVEEHGEVC PANWKGSDTI-D 181
Qy 260 PACKLKFDK 269
Db 182 TPKPEKYSK 191

RESULT 13
AT3385 peroxiredoxin [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AT3385
R;Kaneo, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchii, Nakasaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Accession: AB1807; MUID:21595285; PMID:11759840
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-203 <KUR>
A;Cross-references: GB:BA000019; PIDN:BAB76340.1; PID:g17133778; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr641
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein

RESULT 14
T06318 thiol-specific antioxidant protein precursor homolog TSA - wheat (fragment)
C;Species: Triticum aestivum (common wheat)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 20-Jun-2000
C;Accession: T06318
R;Tsunoyama, Y.
submitted to the EMBL Data Library, January 1997
A;Reference number: Z15590
A;Accession: T06318
A;Status: translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-210 <TSU>
A;Cross-references: EMBL:AB000405; PIDN:BA119099.1
A;Experimental source: cv. Norin-no.61, seedlings
C;Genetics:
A;Gene: TSA
A;Name: nuclear
C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein
C;Keywords: chloroplast
F;1-30/domain: transit peptide (chloroplast) (fragment) #status predicted <TNP>
F;27-169/domain: alkyl hydroperoxidase c22 protein homology <c22>
F;31-210/product: thiol-specific antioxidant protein homolog #status predicted <MAT>
Query Match 40.8%; Score 588.5; DB 2; Length 210;
Best Local Similarity 55.2%; Pred. No. 1.6e-45; Matches 111; Conservative 33; Mismatches 52; Indels 5; Gaps 2;
Matches 111; Conservative 33; Mismatches 52; Indels 5; Gaps 2;

RESULT 15
A47362 thiol-specific antioxidant - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YML028w
C;Species: Saccharomyces cerevisiae
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 11-Jun-1999

C;Accession: A47362; B47362; S49751;
 R;Chae, H.Z.; Kim, I.H.; Kim, K.; Rhee, S.G.
 J. Biol. Chem. 268, 16815-16821, 1993
 A;Title: Cloning, sequencing, and mutation of thiol-specific antioxidant gene of *Saccharomyces cerevisiae*
 A;Reference number: A47362; MUID:93346439; PMID:8344960
 A;Accession: A47362
 A;Molecule type: DNA
 A;Residues: 1-196 <CHA>
 A;Cross-references: EMBL:Z46559; NID:9575680; PIDN:CAA86627_1; PID:9575691
 A;Note: sequence extracted from NCBI backbone (NCBIN:135846, NCBI_P:135847)
 A;Accession: B47362
 A;Molecule type: protein
 A;Residues: 2-13; 62-68; 79-87; 90-94; 137-143; 148-153; 155-160; 192-196 <CH2>
 A;Genetics:
 A;Gene: SGD:TSAL
 A;Cross-references: SGD:S0004490; MIPS:YML028w
 A;Map position: 13J
 C;Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 protein
 C;Keywords: transmembrane protein
 F;2-196/Product: thiol specific antioxidant #status experimental <MAT>
 F;12-153/Domain: alkyl hydroperoxidase c22 protein homology <c22>
 F;34-50/Domain: transmembrane #status predicted <TM>

Query Match
 Best local similarity 55.4%; Score 584; DB 2; Length 196;
 Matches 107; Conservative 33; Mismatches 53; Indels 0; Gaps 0;

Qy 79 AKISKPAPWEGTAVIDEFFKEKLTDYRGKIVVFFFPLDFWVCPBIIAFGDRLEEF 138
 Db 3 AYQKQQAQPFFKKTAWVDCFDEVSIDKKKGKVYVLAFTPLAFYCPCPEITAFSEAKKF 62
 Qy 139 RSINTEVACSVQDFTHAWIITPRROGLGPRIPLSLDTHQISKDYGVYLEDSGHT 198
 Db 63 EEQGAQVLFASTDSEYSLSLAWNINPKGGIGINPLADNHSLSDYGVILLEEGVA 122
 Qy 199 LRGFLIIDKGIIQITNDLPVGRSVDETDLRLVQAOFTDKRGEVSPAGWPGSETIP 258
 Db 123 LRGFLIIDPKGVIRHITINDLPVGRRNDEALRLVAFOWTDKNGTVLPCNNWPGAAIKP 182
 Qy 259 DPAGKLYFDKLN 271
 Db 183 TVEEDSKKEYFEAAN 195

Search completed: January 17, 2003, 19:19:37
 Job time : 24 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model.

Run on: January 17, 2003, 19:15:03 ; Search time 39 Seconds

(without alignments)
925.921 Million cell updates/sec

Title: US-09-911-346-2

Perfect score: 1441
Sequence: 1 MEALPILLAATTTPDHGRHRRLL..... GSETTIPDPAGKLYFDKLN 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470 .

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_101002:*

1: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1980.DAT:*

2: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1981.DAT:*

3: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1982.DAT:*

4: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1983.DAT:*

5: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1984.DAT:*

6: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1985.DAT:*

7: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1986.DAT:*

8: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1987.DAT:*

9: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1988.DAT:*

10: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1989.DAT:*

11: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1990.DAT:*

12: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1991.DAT:*

13: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1992.DAT:*

14: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1993.DAT:*

15: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1994.DAT:*

16: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1995.DAT:*

17: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1996.DAT:*

18: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1997.DAT:*

19: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1998.DAT:*

20: /SIDS2/gcadata/geneseq/geneseq/emb1/AA1999.DAT:*

21: /SIDS2/gcadata/geneseq/geneseq/emb1/AA2000.DAT:*

22: /SIDS2/gcadata/geneseq/geneseq/emb1/AA2001.DAT:*

23: /SIDS2/gcadata/geneseq/geneseq/emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1441	100.0	271	18 AAW12692	Natural killer cell
2	1441	100.0	271	21 AAY43399	Human natural kill
3	1441	100.0	271	22 AAM0249	Human natural kill
4	1441	100.0	271	22 AAB82478	Natural killer cell
5	1441	100.0	271	22 AAB8038	Amino acid sequenc
6	854	59.3	242	22 ABB7947	Drosophila melanog
7	750	52.1	233	21 AAB43528	Human cancer assoc
8	750	52.1	233	23 ABP41353	Human ovarian anti
9	746	51.8	198	22 AAB8036	Amino acid sequenc
10	721	50.0	198	22 AAB8040	Amino acid sequenc

ALIGNMENTS

RESULT	ID	AAW12692 standard; Protein; 271 AA.
AAW12692;	XX	
	XX	
	XX	
05-SEP-1997 (first entry)	XX	
DE Natural killer cell enhancing factor C.	XX	
Natural killer cell enhancing factor C; NKEF C; human; leukaemia cell; natural killer cell; lymphocyte; tumour cell; superoxide radical; LAK; lymphokine-activated killer cell; interleukin-2; growth inhibition; enhanced cell proliferation; antioxidant; vasoactive stromatitis virus; inhibitor; viral infection; inflammation; neoplasia; therapy.	XX	
KW Home sapiens.	XX	
PN WO9639424-A1.	XX	
PN	XX	
12-DEC-1996.	PD	
PF 06-JUN-1995; 95WO-US07200.	XX	
06-JUN-1995; 95WO-US07200.	PR	
(HUMA-) HUMAN GENOME SCI INC.	PA	
Gentz R, Ni J, Rosen CA, Yu G;	PI	
WPI: 1997-043059/04.	DR	
N-P5DB; AAT51788.	XX	

PT DNA encoding human natural killer cell enhancing factor C - useful
PT for preventing or treating viral infections, inflammation, neoplasia
PT and damage from superoxide radicals
XX

PS Claim 1; Fig 1; 61pp; English.

CC This sequence represents the human natural killer cell enhancing factor
CC of NK cells (NK) are a subset of lymphocytes capable
CC of lysing a variety of tumour cells without prior activation.
CC Lymphokine-activated killer cells (LAK) are mainly NK cells activated by
CC interleukin-2, and are capable of lysing wider ranges of tumour cells
CC with higher cytotoxic activity. NK/LAK activity is influenced by various
CC components of blood, including the NKEF A and B proteins. Transfection of
CC NKEF into cells results in cell-type-dependent enhanced cell
CC proliferation or growth inhibition. The NKEF proteins are antioxidants,
CC but show no sequence homology to other antioxidants, such as catalase or
CC superoxide dismutase. This sequence, or the DNA encoding it can be used
CC to inhibit the cytopathic effect of vesicular stomatitis virus and to
CC inhibit the growth of leukaemia cells, or to treat a patient in need of a
CC NKEF C polypeptide. Disease or a susceptibility to disease related to an
CC under-expression of this protein can be diagnosed by determining a
CC mutation in the DNA encoding this sequence. This protein can also be used
CC to identify compounds which bind to and activate a receptor for it. The
CC products can also be used to treat viral infections, inflammation,
CC neoplasia and damage from superoxide radicals.

SQ Sequence 271 AA;

Query Match	100 %	Score	1441	DB	18	Length	271;
Best Local Similarity	100.0%	Pred. No.	1.4e-147				
Matches	271;	Conservative	0;	Mismatches	0;	Indels	0;
							Gaps 0;

QY 1 MEALPLLAATTPDGHRRRLPLPLFLPAGAVQWEGTAVIDGEREFKELKLTDRGKYLVFFFPLDF 120

Db 1 MEALPLLAATTPDGHRRRLPLPLFLPAGAVQWEGTAVIDGEREFKELKLTDRGKYLVFFFPLDF 60

QY 61 PGESRVSVAHDHSLHSKAKSKPAPYWGTAVIDGEFEFLKLDRGKYLVFFFPLDF 120

Db 61 PGESRVSVAHDHSLHSKAKSKPAPYWGTAVIDGEFEFLKLDRGKYLVFFFPLDF 60

QY 121 TFWCPTTEIAFGDRLEEFRSINTEVVACSVSDVSQFTLAWINTPRROGLGPIRPLSDL 180

Db 121 TFWCPTTEIAFGDRLEEFRSINTEVVACSVSDVSQFTLAWINTPRROGLGPIRPLSDL 180

QY 181 THOISKDGYVYLEDSGHTLRLFIDDKGLRQITNDLPVGRSVDETLRLVQAFQYTDK 240

Db 181 THOISKDGYVYLEDSGHTLRLFIDDKGLRQITNDLPVGRSVDETLRLVQAFQYTDK 240

QY 241 HGEVCPAGWKPGSETIIPDPAGKLKYFDKLN 271

Db 241 HGEVCPAGWKPGSETIIPDPAGKLKYFDKLN 271

RESULT 2

AY43399 ID AY43399 standard; Protein: 271 AA.

AC AY43399;

XX DT 28-JAN-2000 (first entry)

DE Human natural killer cell enhancing factor C protein sequence.

XX KW Natural killer cell enhancing factor C; NKEF C; human; diagnosis; probe;
KW viral infection; inflammation; neoplasia; superoxide radical damage;
KW bone marrow rejection; therapy.

OS Homo sapiens.

XX PN US595612-A.

XX PD 16-NOV-1999.

PF 06-JUN-1995; 95US-0467265.

PT XX PR 06-JUN-1995; 95US-0467265.

PA XX PA (YUGG/) YU G.
PA (ROSSE/) ROSEN C.A.
PA (NIJU/) NI J.

PI Gentz R., Rosen CA, Yu G, Ni J;

XX DR WPI: 2000-012791/01.
N-PSDB, AR237242.

XX CC Isolated polynucleotides encoding human natural killer cell enhancing
PT factor C, useful for preventing, diagnosing or treating viral
infections, neoplasia and damage from superoxide radicals -

XX PS Claim 1; Fig 1; 29pp; English.

CC This sequence is the human natural killer cell enhancing factor C
CC (NKEF C) of the invention. NKEF C protein and DNA sequences can be used
CC in the diagnosis, prevention and treatment of disorders associated with
CC inappropriate expression and activity (normally reduced) of NKEF C and to
CC augment the action of natural killer cells and proteins. The NKEF C
CC sequences may be used to treat disorders such as viral infections,
CC administered to treat the above diseases by rectifying mutations or
deletions in a patient's genome that affect the activity of NKEF C by
CC expressing inactive proteins or to supplement the patient's own production
CC of NKEF C. Antisense nucleic acid molecules may be administered to down
regulate NKEF C expression by binding with the cell's own NKEF C genes and
preventing their expression. The NKEF C DNA and antisense molecules may
also be used as probes in diagnostic assays to detect and quantitate the
presence of similar nucleic acid sequences in samples, and hence which
patients may be in need of restorative therapy. They may also be used to
study the expression and function of NKEF C and its role in metabolism.
NKEF C fragments may be used as antigens in the production of antibodies
against NKEF C and in assays to identify modulators (agonists and
antagonists) of NKEF C expression and activity. Anti-NKEF C antibodies
and NKEF C antagonists may also be used to down regulate NKEF C
expression and activity. They may be used in this way to treat disorders
such as the treatment of bone marrow rejection. The antibodies may also
be used as diagnostic reagents for identifying the presence of NKEF C in
samples.

SQ Sequence 271 AA;

Query Match	100 %	Score	1441	DB	21	Length	271;
Best Local Similarity	100.0%	Pred. No.	1.4e-147				
Matches	271;	Conservative	0;	Mismatches	0;	Indels	0;
							Gaps 0;

QY 1 MEALPLLAATTPDGHRRRLPLPLFLPAGAVQWEGTAVIDGEREFKELKLTDRGKYLVFFFPLDF 120

Db 1 MEALPLLAATTPDGHRRRLPLPLFLPAGAVQWEGTAVIDGEREFKELKLTDRGKYLVFFFPLDF 60

QY 61 PGESRVSVAHDHSLHSKAKSKPAPYWGTAVIDGEFEFLKLDRGKYLVFFFPLDF 120

Db 61 PGESRVSVAHDHSLHSKAKSKPAPYWGTAVIDGEFEFLKLDRGKYLVFFFPLDF 180

QY 121 TFWCPTTEIAFGDRLEEFRSINTEVVACSVSDVSQFTLAWINTPRROGLGPIRPLSDL 180

Db 121 TFWCPTTEIAFGDRLEEFRSINTEVVACSVSDVSQFTLAWINTPRROGLGPIRPLSDL 180

QY 181 THOISKDGYVYLEDSGHTLRLFIDDKGLRQITNDLPVGRSVDETLRLVQAFQYTDK 240

Db 181 THOISKDGYVYLEDSGHTLRLFIDDKGLRQITNDLPVGRSVDETLRLVQAFQYTDK 240

QY 241 HGEVCPAGWKPGSETIIPDPAGKLKYFDKLN 271

Db 241 HGEVCPAGWKPGSETIIPDPAGKLKYFDKLN 271

RESULT 3

ID AAM50249 standard; Protein; 271 AA.

XX

AC AAM50249;

DT 21-JAN-2002 (first entry)

DE Human natural killer cell enhancing factor C.

XX

Natural killer cell enhancing factor C; NKEF C; human; antiviral; virucide; antiinflammatory; cytoprotective; antioxidant; vulnerable; therapy; diagnosis.

KW

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..30 /label= Signal_peptide

FT Protein 31..271 /label= Mature_protein

XX

US6294164-B1.

XX

PD 25-SEP-2001.

PF 29-SEP-1999; 99US-0407891.

XX

PR 06-JUN-1995; 95US-0467265.

PA (HUMA-) HUMAN GENOME SCI INC.

PT NI J., Yu G., Gentz R., Rosen CA;

XX

DR WPI; 2001-647258/774.

DR N-PSDB; AAI70524.

XX

PT Natural killer cell enhancing factor C polypeptides encoded by the cDNA in ATCC Deposit No. 97157, useful for preventing or treating viral infections, inflammation, neoplasia or damage from superoxide radicals, e.g. tissue injury.

PT

XX

PS Claim 1; FIG 1; 29pp; English.

XX

The present sequence is that of human natural killer cell enhancing factor C (NKEF C), as deduced from a cDNA clone (see AAI70524) isolated from a cDNA library derived from cyclohexamide-treated CEM cells. NKEF C is structurally related to highly conserved oxidative stress proteins and shows 68% identity and 83% similarity to NKEF B. NKEF C is highly expressed in heart, liver, skeletal muscle, pancreas, testis and ovary, moderately expressed in placenta, lung, prostate, small intestine and colon, and lowly expressed in brain, spleen, thymus and peripheral blood leucocytes. NKEF C polypeptide is useful for preventing and/or treating viral infections, inflammation, neoplasia or damage from superoxide radicals (e.g. tissue injury or ageing). The polypeptide may also be used for inhibiting the cytopathic effect of vesicular stomatitis virus and for inhibiting the growth of leukaemia cells. The polypeptide and polynucleotide are also useful as research reagents, for constructing DNA vectors, and for developing therapeutics and diagnostics for treating human disease. Polypeptide fragments of NKEF C that have growth inhibitory or antiviral activity are claimed.

XX

Sequence 271 AA:

100.0%; Score 1441; DB 22; Length 271;

Best Local Similarity 100.0%; Pred. 1.4e-147; Mismatches 0; Indels 0; Gaps 0;

Matches 271; Conservative 0;

QY 1 MEALPLLAATPDPHGRHLRLPLPLFLPLPAGAVQWETEPRTRREECHFYAGQVY 60

Db 1 MEALPLLAATPDPHGRHLRLPLPLFLPLPAGAVQWETEPRTRREECHFYAGQVY 60

1 MEALPLLAATPDPHGRHLRLPLPLFLPLPAGAVQWETEPRTRREECHFYAGQVY 60

RESULT 4

QY 61 PGEASRVSDADSLHLISKAKTSKPKAPWEGTAVIDGEGFKELKLTDYRGKVIVFFFVPLDF 120

Db 61 PGEASRVSDADSLHLISKAKTSKPKAPWEGTAVIDGEGFKELKLTDYRGKVIVFFFVPLDF 120

XX

AC AAB82478;

DT 22-AUG-2001 (first entry)

DE Natural killer cell enhancing factor C.

XX

Natural killer cell enhancing factor C; NKEF C; human; antioxidant; virucide; antiinflammatory; virucide; antitumour; therapy; diagnosis.

KW

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..30 /label= Signal_peptide

FT Protein 31..271 /label= Mature_protein

XX

US6255079-B1.

XX

PD 03-JUL-2001.

PF 06-JUN-1995; 95US-0467265.

XX

PR 06-JUN-1995; 95US-0467265.

PA (HUMA-) HUMAN GENOME SCI INC.

PT NI J., Yu G., Gentz R., Rosen CA;

XX

DR WPI; 2001-396982/42.

DR N-PSDB; AAF0573.

XX

PT Isolated polynucleotides encoding human natural killer cell enhancing factor C, useful for preventing, diagnosing or treating viral infections, neoplasia and damage from superoxide radicals -

XX

PS Claim 1; Fig 1; 49pp; English.

XX

The present sequence is that of human natural killer cell enhancing factor C (NKEF C). NKEF C is highly expressed in heart, liver, skeletal muscle, pancreas, testis and ovary, moderately in placenta, lung, prostate, small intestine and colon, and lowly expressed in brain, spleen, thymus and peripheral blood leukocytes. cDNA (see AAF0573) encoding NKEF C was derived from cyclohexamide-treated CEM cells. The protein shows 83.3% amino acid similarity to NKEF B, and shows significant homology to several other proteins (thiol-specific antioxidants) from a wide range of organisms. The invention provides NKEF C polypeptides, especially a polypeptide comprising amino acids 1-271, or 31-271 of the present sequence, isolated nucleic acids encoding them, and methods

CC of producing the polypeptides in recombinant host cells. The NKEF
 CC C polypeptides and polyuridylates can be used to inhibit the
 CC growth of leukaemia cells, to treat viral infection, to augment the
 CC effects of NK protein, to treat neoplasias such as tumours and
 CC cancers, to prevent inflammation, and to prevent damage from
 CC superoxide radicals in the body e.g. in tissue injury and ageing.
 CC The polypeptides can also be used to screen for potential agonists
 CC and antagonists of NKEF C activity. Antagonists may be useful in
 XX the treatment of bone marrow transplant rejection.

Sequence 271 AA;

Query Match 100.0%; Score 1441; DB 22; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1.4e-147;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEALPLAATPDHGRRHLRLPLFLPAGAVQGWETEERPRTREECHFVAGQVY 60
 Db 1 MEALPLAATPDHGRRHLRLPLFLPAGAVQGWETEERPRTREECHFVAGQVY 60

Qy 61 PGEASRVSDADHSIHLSKAKISKAPWYGMGTAVIDGEFELKLTIDYRGKLYVFFYPLDF 120
 Db 61 PGEASRVSDADHSIHLSKAKISKAPWYGMGTAVIDGEFELKLTIDYRGKLYVFFYPLDF 120

Qy 121 TFCVCPTEITAFGORLEERSINTEWVACSVDSOFTLAWINTPRROQGLGPIRIPPLSDL 180
 Db 121 TFCVCPTEITAFGORLEERSINTEWVACSVDSOFTLAWINTPRROQGLGPIRIPPLSDL 180

Qy 181 THQISKDGYVYLEDSGHTLRGLFIDDKGILRQITNDLPGRSVDETLRLVQAFQYTDK 240
 Db 181 THQISKDGYVYLEDSGHTLRGLFIDDKGILRQITNDLPGRSVDETLRLVQAFQYTDK 240

Qy 241 HGEVCAGWKPGSETITPDAGKLKFDFKLN 271
 Db 241 HGEVCAGWKPGSETITPDAGKLKFDFKLN 271

RESULT 5

ID AAB68038
 ID AAB68038 standard; Peptide; 271 AA.

AC AAB68038;
 XX
 AC
 XX
 DT 29-JUN-2001 (first entry)

DE Amino acid sequence of the acid form of peroxiredoxin TDXX.
 DE
 XX
 KW Peroxiredoxin; acid form; oxidative stress; cell death; cancer;
 KW autoimmune disease; neurodegeneration; metabolic disorder.
 OS Homo sapiens.

PN FR2798672-A1.
 XX
 XX
 PD 23-MAR-2001.

PF 17-SEP-1999; 99FR-0011663.
 XX
 PR 17-SEP-1999; 99FR-0011663.

(COMS) COMMISSARIAT ENERGIE ATOMIQUE.
 PI Rabilloud T;
 XX
 DR WPI; 2001-259869/27.

PT Purified acid form of peroxiredoxin, a marker of oxidative stress,
 PT useful in diagnosis and for identifying potential apoptotic and
 PT anti-apoptotic agents comprises a specific amino acid motif close to
 XX the active site -
 PS Claim 12; Page 23-24; 28pp; French.

CC The present sequence represents the acid form of a human peroxiredoxin
 CC enzyme. The acid form of peroxiredoxin is a characteristic marker of
 CC oxidative stress that can be measured simply and quickly, providing a
 CC reliable indication of stress even where this is of short duration.
 CC Modulators of the acid form of peroxiredoxin enzyme are used for the
 CC stimulation or inhibition of apoptosis. Compounds that stimulate
 CC formation of the acid form of peroxiredoxins are used to induce cell
 CC death (treatment of cancer and autoimmune diseases) while those that
 CC inhibit its formation are used to prevent cell death (treatment of
 CC neurodegeneration). Measuring the ratio between acid form and the native
 CC form of peroxiredoxin is used to diagnose metabolic disorders associated
 XX with oxidative stress.

Sequence 271 AA;

Query Match 100.0%; Score 1441; DB 22; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1.4e-147;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEALPLAATPDHGRRHLRLPLFLPAGAVQGWETEERPRTREECHFVAGQVY 60
 Db 1 MEALPLAATPDHGRRHLRLPLFLPAGAVQGWETEERPRTREECHFVAGQVY 60

Qy 61 PGEASRVSDADHSIHLSKAKISKAPWYGMGTAVIDGEFELKLTIDYRGKLYVFFYPLDF 120
 Db 61 PGEASRVSDADHSIHLSKAKISKAPWYGMGTAVIDGEFELKLTIDYRGKLYVFFYPLDF 120

Qy 121 TFCVCPTEITAFGORLEERSINTEWVACSVDSOFTLAWINTPRROQGLGPIRIPPLSDL 180
 Db 121 TFCVCPTEITAFGORLEERSINTEWVACSVDSOFTLAWINTPRROQGLGPIRIPPLSDL 180

Qy 181 THQISKDGYVYLEDSGHTLRGLFIDDKGILRQITNDLPGRSVDETLRLVQAFQYTDK 240
 Db 181 THQISKDGYVYLEDSGHTLRGLFIDDKGILRQITNDLPGRSVDETLRLVQAFQYTDK 240

Qy 241 HGEVCAGWKPGSETITPDAGKLKFDFKLN 271
 Db 241 HGEVCAGWKPGSETITPDAGKLKFDFKLN 271

RESULT 6

ID ABB57947
 ID ABB57947 standard; Protein; 242 AA.

AC ABB57947;
 XX
 AC
 XX
 DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 633.
 DE
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.
 XX
 PD 27-SEP-2001.

XX
 XX
 PF 23-MAR-2001; 2001WO-US09231.

XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.

XX
 PA (PEKE) PE CORP NY.

XX
 PA Venter J.C., Adams M., Li P.W.D., Myers E.W.;

XX
 DR WPI; 2001-656860/75.

XX
 DR N-ISDB; ABL02050.

XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 genes from Drosophila and for elucidating cell signalling and cell-cell

PT interactions -
 XX
 Disclosure; SEQ ID NO 633; 21pp + Sequence listing; English.
 PS
 XX
 CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB116176-ABL130511), expressed DNA sequences (AB011840-ABL6175) and the encoded proteins (ABB7737-ABB7207).
 CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX SQ Sequence 242 AA;
 Query Match 59.3%; Score 854.5; DB 22; Length 242;
 Best Local Similarity 65.2%; Pred. No. 4.5e-84; Mismatches 48; Indels 9; Gaps 2;
 Matches 161; Conservative 29; Mismatches 48; Indels 9; Gaps 2;
 QY 25 LLLFLPILPAGAVQGWEETEPRTREREBCFHAGQVYPGEASRSVADHSIHLSSAKISKP 84
 Db 5 LSVLLSAAALVGAAKPED----NSCYSHSAGGSYVPDQPK---GDHQIQQYKAVISKP 55
 QY 85 APYWEGTAVTIDGEKFKEKLKDYRGKLYVFFYPLDFTEVCPTEIAFGDLEERSINTE 144
 Db 56 AQPQFEGTAVVNKEVKLSSLSQLGKVWLLFYPPLDFTFVCPTEIAFSDRIAFEKKITE 115
 QY 145 WVACCVSDQSQTPLAWINTPREGGLGPIRPLSDITHQTSKDXGYVLEDGHTURGLEI 204
 Db 116 VIGVSVDSHFTHLAWINTPREGGLGDKVPLSDLTHKISKDYGVYLESGHALRGLFI 175
 QY 205 IDDKGILRQLQTTLNDLPVGRSVDETLRLVQAFQYTDTHGEVCPCAGKPGSETITIPDPAGKL 264
 Db 176 IDTCGYLRLQITMNDLPVGRSVDETLRLVQAFQYTDTHGEVCPCAGKPGSETITIPDPAGKL 235
 QY 265 KYFDKLN 271
 Db 236 KYFKANN 242
 RESULT 7
 AAB43528
 ID AAB43528 standard; Protein; 233 AA.
 XX
 AC AAB43528;
 XX
 DT 08-FEB-2001 (first entry)
 DE Human cancer associated protein sequence SEQ ID NO:973.
 XX
 KW Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cyrostatic; proliferative; pulmonary; immunomodulator; antidiabetic; antiasthmatic; antireumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antiallergic; antihypertensive; antidiarrhoeal; antitussive; antiparasitic; antidiabetic; antihypertensive; antidiarrhoeal; antitussive; antiparasitic; dermatological; neuroprotective; cardiotonic; antidiarrhoeal; antitussive; antiparasitic; antidiabetic; antihypertensive; antidiarrhoeal; antitussive; antiparasitic; vasotropics; antipsoriatic; antidiarrhoeal; antitussive; antiparasitic; dermatological; neuroprotective; cardiotonic; antidiarrhoeal; antitussive; antiparasitic; antidiabetic; antihypertensive; antidiarrhoeal; antitussive; antiparasitic; immune disorder; haemopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
 OS Homo sapiens.
 XX
 PN WO200055350-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US05882.
 XX
 PR 12-MAR-1999; 99US-0124270.

XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX DR WPI: 2000-58753/55.
 XX N-PSDB; AAC7737.
 CC Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer -
 PT
 XX Claim 11; Page 1542-1543; 235pp; English.
 CC AAC77607 to ACT78448 encode the human cancer associated proteins given in AB4339 to AAB4429. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; CC antidiabetic; antiasthmatic; antihypertensive; antiarhythmic; CC antifibrillatory; anitthyroid; antiallergic; antibacterial; antiviral; CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant; CC nootropic; vasotropic; antiparasitic and antiangiogenic. The CC polynucleotides and polypeptides can be used for preventing, treating or CC ameliorating medical conditions and diagnosing pathological conditions. CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from CC the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of CC immune cells, to treat disorders of haematopoietic cells, autoimmune CC disorders, allergic reactions, graft versus host disease and organ CC rejection, modulate haemostatic or thrombolytic activity, modulate CC inflammation, cancers, cardiovascular disorders, neurological disease and CC bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. Act78449 to CC AAC78457 and AAB42420 represent sequences used in the exemplification of CC the present invention.
 XX SQ Sequence 233 AA;
 Query Match 52.1%; Score 750.5; DB 21; Length 233;
 Best Local Similarity 67.1%; Pred. No. 8e-73; Mismatches 40; Indels 1; Gaps 1;
 Matches 139; Conservative 27; Mismatches 40; Indels 1; Gaps 1;
 QY 64 ASRVSVADHSIHLSSAKISKPAPYNGEVTI-DGFKEKLKDYRGKLYVFFYPLDFE 122
 Db 25 ATCGVGTADRKMSGSNAKIGHPAPNPKATAYMPDSQPKDISLSDYKGKVYFFFPLDFE 84
 QY 123 VCPTEIAFGDLEERSINTEVVACSVDSOFTLAWINTPREGGLGPIRPLISDLTH 182
 Db 85 VCPTEIAFGDLEERSINTEVVACSVDSOFTLAWINTPREGGLGPIRPLISDLTH 144
 QY 183 QISKDGYVYLEDGHTURGLEIIDDKGILRQLITNLDPVGRSVDETLRLVQAFQYTDKG 242
 Db 145 TIAQDGVLRADEGTSFRGFLIEDDKGILRQLITNLDPVGRSVDETLRLVQAFQYTDKG 204
 QY 243 EVCPAGWKPGSETITDPACKLKYDK 269
 Db 205 EVCPAGWKPGSETITDPACKLKYDK 231
 RESULT 8
 ABP41353
 ID ABP41353 standard; Protein; 233 AA.
 XX
 AC ABP41353;
 XX
 DT 23-AUG-2002 (first entry)
 DE Human ovarian antigen HCO001, SEQ ID NO:2485.
 XX
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;

KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cyostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive; chromosome 1p34.1.
 OS Homo sapiens.

XX WO200200677-A1.
 XX PR 07-JUN-2001; 2001WO-US18569.
 XX PD 03-JAN-2002.
 XX PR 07-JUN-2000; 2000US-209467P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 PI Birse CE, Rosen CA;
 XX DR WPI; 2002-147878/79.
 DR N-PSDB; ABQ4430.
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g., ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases -
 XX PS Claim 11; SEQ ID No 2485; 2922pp; English.
 XX CC The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ4131-ABQ6305), and also encompasses polypeptides 90% identical and poly nucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vector and host cells comprising human ovarian antigen poly nucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen poly nucleotides and polypeptides in diagnosing, treating, prognosis or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility), disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea, endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis), and toxic shock syndrome, inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and poly nucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The poly nucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 233 AA;

Query Match 52.1%; Score 750.5; DB 23; Length 233;
 Best Local Similarity 67.1%; Pred. No. 8e-73; Mismatches 139; Conservative 27; Indels 1; Gaps 1;

QY 64 ASRVADHSLHLSKAKISKPKAPYWEGRPAVIFGERELKLKDYRGKLVLFVFFYLDPDFTF 122
 Db 25 ACGVGTADRKMSGGNAIGHPAPNFKTAVMPDGQFDISLDYKSKYVWFYPLDFTF 84

QY 123 VCPTEITAFGDRIEEFISINTEVACVDSQFLHAWINTRRQGGGPIRPLSLDLTH 182
 Db 85 VCPTEITAFSDFRAEFLKLNCQVIGASVDSFLHAWINTPRQGGGPMLPILSDPKR 144

XX Sequence 198 AA;

Query Match 51.8%; Score 746; DB 22; Length 198;
 Best Local Similarity 70.5%; Pred. No. 2e-72; Mismatches 136; Conservative 26; Indels 0; Gaps 0;

QY 79 AKTSKAPYWEGRPAVIFGERELKLKDYRGKLVLFVFFYLDPDFTFVCTEITAFGDRLEEF 138
 Db 6 LARIKGPAFDKATAFVVGAFKEVLSKDSYKGVYVLFYPLDFTFVCPTEITAFSRAEDF 65

QY 139 RSINTEVACVDSQFLHAWINTPRQGGGPMLPILSDPKR 198
 Db 66 RKLGEVLFVSYDSQFLHAWINTPRQGGGPMLPILSDPKR 125

Qy	199 LRGLFTIDDKGILRQITLNDLPGVGRSVDETLRLVQAFOYTDKHGEVCPAGWKPGSETIIP 258	Db	: : : : : : : : : :
Db	126 YRGLFTIDDKGILRQITLNDLPGVGRSVDETLRLVQAFOYTDKHGEVCPAGWKPGSETIIP 185	Qy	258 PDPAGKLKYDK 269
Qy	259 DPAGKLKYDKLN 271	Db	185 PDVOKSKYFSK 196
Db	186 NVDDSKEYFSKH 198		
	RESULT 10		
AAB6040	AAB6040 standard; peptide; 198 AA.	AAB78580	AAU78580 standard; Protein; 198 AA.
ID	AR6040;	ID	AAU78580;
XX		XX	
AC		AC	AAU78580;
XX		XX	
DT	29-JUN-2001 (first entry)	DT	05-JUN-2002 (first entry)
XX		XX	
DE	Amino acid sequence of the acid form of peroxiredoxin TDx2.	DE	Mouse peroxiredoxin II-1 (PrxII-1) protein.
XX		XX	
DE	Peroxiredoxin; acid form; oxidative stress; cell death; cancer;	KW	Peroxiredoxin; Prx; promoter; PrxII-1.
XX		KW	
KW	autoimmune disease; neurodegeneration; metabolic disorder.	OS	Mus sp.
XX		OS	
OS	Homo sapiens.		
XX			
PN	FR2798672-A1.	FN	Key Location/Qualifiers
XX		FT	Misc-difference 7 /note= "Encoded by CAA"
PD	23-MAR-2001.	FT	Misc-difference 97 /note= "Encoded by GGC"
XX		XX	
PF	17-SEP-1999; 99FR-0011663.	PR	KR99066020-A.
XX		XX	
PR	17-SEP-1999; 99FR-0011663.	PD	16-AUG-1999.
XX		XX	
PA	(COMS) COMMISSARIAT ENERGIE ATOMIQUE.	PA	20-JAN-1998; 98KR-0001604.
XX		XX	
PI	Rabilloud T;	PR	20-JAN-1998; 98KR-0001604.
XX		XX	
DR	Rabilloud T;	PA	(KOAD) KOREA ADV INST SCI & TECHNOLOGY.
XX		XX	
PS	Claim 12; Page 25-26; 28pp; French.	PT	Yeom YI, Lim MJ, Lee GG, Yoo DY;
XX		XX	
CC	The present sequence represents the acid form of a human peroxiredoxin enzyme. The acid form of peroxiredoxin is a characteristic marker of oxidative stress that can be measured simply and quickly, providing a reliable indication of stress even where this is of short duration.	DR	WPI; 2000-547264/50.
CC	Modulators of the acid form of peroxiredoxin enzyme are used for the formation or inhibition of apoptosis. Compounds that stimulate formation of the acid form of peroxiredoxins are used to induce cell death (treatment of cancer and autoimmune diseases) while those that inhibit its formation are used to prevent cell death (treatment of neurodegeneration). Measuring the ratio between acid form and the native form of peroxiredoxin is used to diagnose metabolic disorders associated with oxidative stress.	DR	N-PSDB; ABK47315.
CC		XX	
CC		PT	Peroxiredoxin PRX II-1 and promoter derived from mouse, base sequence of PRX II-2 and PRX II-3 -
CC		XX	
PS	Disclosure; Fig 6; 14pp; English.	PS	This invention relates to the sequence of the mouse peroxiredoxin II-1 (PrxII-1) promoter. The invention also comprises the cDNA sequences encoding the mouse PrxII-1, PrxII-2 and PrxII-3 proteins. The present sequence represents the mouse peroxiredoxin protein sequence of the invention.
SQ	Sequence 198 AA:	Qy	79 AKISKPAPYWEGTAVIDGEKFRELKJUDRGKYLVFIFYPLDFTFCPTETIAFGDRLEE 137
SQ	Sequence 198 AA:	Qy	139 RSINTEVVACSDQSFTHLAWINTPQQGGPPIRPLSLDTHQISDKYGYLEDSGHT 198
Query Match	50.0%; Score 721; DB 22; Length 198;	Qy	79 AKISKPAPYWEGTAVIDGEKFRELKJUDRGKYLVFIFYPLDFTFCPTETIAFGDRLEE 138
Best Local Similarity	69.8%; Pred. No. 1; Le-69; 31; Indels 2; Gaps 2;	Db	6 AHIGKSAPPDTAVWDVGAFKEIKLSRDGYKVWLFYPLDFTFCPTETIAFGDRLEE 65
Matches	134; Conservative 25; Mismatches 31; Indels 2; Gaps 2;	Qy	139 RSINTEVVACSDQSFTHLAWINTPQQGGPPIRPLSLDTHQISDKYGYLEDSGHT 199
Oy	79 AKISKPAPYWEGTAVIDGEKFRELKJUDRGKYLVFIFYPLDFTFCPTETIAFGDRLEE 137	Db	66 RKLGFITDDKGILRQITLNDLPGVGRSVDETLRLVQAFOYTDKHGEVCPAGWKPGSETIIP 125
Db	6 AKIGHPAPNPKATAVMDQGFFKDISLDYKGVWVFIFYPLDFTFCPTETIAFGDRLEE 65	Qy	139 RSINTEVVACSDQSFTHLAWINTPQQGGPPIRPLSLDTHQISDKYGYLEDSGHT 199
Oy	138 FRSINTEVVACSDQSFTHLAWINTPQQGGPPIRPLSLDTHQISDKYGYLEDSGHT 197	Qy	199 LRGLFTIDDKGILRQITLNDLPGVGRSVDETLRLVQAFOYTDKHGEVCPAGWKPGSETIIP 258
Db	66 FRKLNCQVIGASVDSHFLAWNTPKQGGLGPMNIPLVSPKRTIAQDYGGVLADEGI 125	Db	126 YRGLFTIDDKGILRQITLNDLPGVGRSVDETLRLVQAFOYTDKHGEVCPAGWKPGSETIIP 185
Qy	198 TURGLFTIDDKGILRQITLNDLPGVGRSVDETLRLVQAFOYTDKHGEVCPAGWKPGSETIIP 257	Qy	259 DPAGKLKYDFKL 271

Db	186	NVDDSKEYFSKHN	198
RESULT	12	:	
ID	ABB58322	ABB58322 standard; Protein; 194 AA.	
XX			
AC	ABB58322;		
XX			
DT	26-MAR-2002	(first entry)	
XX			
DE	Drosophila melanogaster polypeptide SEQ ID NO 1758.		
KW	Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.		
XX			
OS	Drosophila melanogaster.		
XX			
PN	WO200171042-A2.		
XX			
PD	27-SEP-2001.		
XX			
PF	23-MAR-2001; 2001WO-US09231.		
PR	23-MAR-2000; 2000US-191637P.		
XX	11-JUL-2000; 2000US-0614150.		
PA	(PEKE) PE CORP NY.		
XX			
PI	Venter JC, Adams M, Li PWD, Myers EW;		
XX			
DR	WPI; 2001-656860/75.		
DR	N-PSDB; ABL02425.		
XX			
PS	New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -		
XX			
PS	Disclosure; SEQ ID NO 1758; 21pp + Sequence Listing; English.		
XX			
PT	The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL3051), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABL57737-ABB22072).		
CC	The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences .		
CC			
SQ	Sequence 194 AA:		
Query Match	Best Local Similarity 49.6%; Score 715; DB 22; Length 194; Matches 129; Conservative 29; Mismatches 31; Indels 0; Gaps 0;		
QY	80 KISKPAWPWEGTAVIDGEFKELKLTDYRGKLYVFFYPLDFTFVCPTETIAGFDRLEEFR 139		
Db	3 QLQKPAFPAGTAWVNGVFKDILSDKGKIVLFFFPLDFTFVCPTETIAGFDRLEEFR 62		
QY	80 KISKPAWPWEGTAVIDGEFKELKLTDYRGKLYVFFYPLDFTFVCPTETIAGFDRLEEFR 139		
Db	3 QLQKPAFPAGTAWVNGVFKDILSDKGKIVLFFFPLDFTFVCPTETIAGFDRLEEFR 62		
QY	140 SINTEVVACSVSDFQTHLAWINPFRROGGLPRTIPILSDLTHOTSKDGYLGLEDSGHTL 199		
Db	63 KINCEVIGCSTDQSFTHLAWINPFRKGGLGSMDIPLADKSMKVARDYGVLDDEERGIPF 122		
QY	200 RGLFIIDDKGILRQITNDLPGRSVDETLRLVQAQYTDKHEGEVCPAGWPKGSETIIPD 259		
Db	123 RGLFIIDDKQNLRQITNDLPGVRSVEETRLVQAFQYTDKHEGEVCPANWPKGQKTMWAD 182		
QY	260 PAGKLKYFD 268		
QY	: :		

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Page 10

Db :| |||| |||| |:||||||| :| ||| :| ||||| |||:||| ||| ||| |||
93 VNCCEVVAVSVDSHESHLAWINTPRKGGLGHMNTAALSDLJKQISRDYGVILESGLAIR 152
Qy 201 GLFIDDDKGILRQTILNDLPVGRSYDETLRLVQAFQYTDKIGEVCPAGWKGSEPTIPDP 260
Db ||||| ^:::||||| :| ||| ||| ||| ||| ||| ||| ||| ||| |||
153 GLFIDDPNGVIKHLNSNDLPGRSVEETLRUVKAQYVETHEVCPANWFPSPIKSP 212
Qy 261 AGKLKYFDKLN 271
Db | :|| |:
213 RASKEYFOKVN 223

Search completed: January 17, 2003, 19:18:23
Job time : 41 secs

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Om protein - protein search, using sw model.

Run on: January 17, 2003, 19:16:47 ; Search time 35 Seconds

(without alignments) (without alignments) (without alignments)
1595.393 Million cell updates/sec

Title: US-09-911-346-2

Perfect score: 1441

Sequence: I MEALFLLAATTDPDHRRHRL.....GSEFTIPDPAGKLKYFDKLN 271

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : SPTREMBL_21;*

- 1: sp_archea;*
- 2: sp_bacteria;*
- 3: sp_fungi;*
- 4: sp_human;*
- 5: sp_invertebrate;*
- 6: sp_mammal;*
- 7: sp_mhc;*
- 8: sp_organelle;*
- 9: sp_phage;*
- 10: sp_plant;*
- 11: sp_rabbit;*
- 12: sp_virus;*
- 13: sp_vertebrate;*
- 14: sp_unclassified;*
- 15: sp_rvirus;*
- 16: sp_bacteriophage;*
- 17: sp_archaea;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT	ID	Description	PR%;	PR%;	PR%;	PR%;
1	Q9SGI2	PRELIMINARY;				274 AA.
	Q9SGI2;					
		01-JUN-2001 (TREMBLrel. 17, Created)				
		DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
		DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
		PEROXIREDOXIN				
		Bos taurus (Bovine)				
		OS Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;				
		OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;				
		OC Bovidae; Bovinae; Bos.				
		OX NCBI-TAXID=9913;				
		RN [1]				
		RP SEQUENCE FROM N.A.				
		RC TISSUE=LIVER;				
		RA Levens G., Donnay I., Knops B.;				
		RT "Cloning of 4 new bovine peroxiredoxins, and screening of the complete peroxiredoxin family in different bovine tissues";				
		RT Submitted (SPR-2000) to the EMBL/GenBank/DBJ databases.				
		RL Submitted (SPR-2000) to the EMBL/GenBank/DBJ databases.				
		DR EMBL; AR305563; ARGS3660.1; -.				
		DR PR0041; 1PRX.				
		DR InterPro; IPR00866; AIPC-TSA.				
		DR Pfam; PF00578; AIPC-TSA; 1.				
		SEQUENCE 274 AA; 30741 MW: AEI4176CF1C70E37 CRC64;				

Query	Match	Length	DB ID	Description
Q9gq12	bos taurus	274	6 Q9BG12	
Q9gq12	rattus norvegicus	273	11 Q9Z0V5	
Q9gq12	biomphalaria	223	5 Q9BF6	
Q9gq12	drosophila	242	5 Q9V04	
Q9gq12	bos taurus	199	6 Q9BG13	
Q9gq12	globodera rufa	199	5 Q9Y82	
Q9gq12	mus musculus	198	11 Q9WJ4	
Q9gq12	mus musculus	198	11 Q88376	
Q9gq12	cricetulus	199	11 Q9JKY1	
Q9gq12	bos taurus	199	6 Q9BG14	
Q9gq12	cyprinus carpio	199	13 Q93241	
Q9gq12	ascaris suum	195	5 Q9N198	
Q9gq12	mus musculus	198	11 Q9BW12	
Q9gq12	mus musculus	196	5 Q9B49	
Q9gq12	aegyptiaca	196	5 Q8wsf6	
Q9gq12	drosophila	194	5 Q9V3P0	

Db	128	PTEILAFGDRIDERSINTEVACSVSDSQTFLHANIINTPRQGLGSINIPPLADLNHQI	187	OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
Qy	185	SKDYGVYLEDSGHTRLGLFTIDDKGILTROITLNDLPGVRSVDETLRVQAFQYTDKHEV	244	OC	Planorbidae; Biomphalaria.
Db	188	SKDYGVYLEDSGHTRLGLFTIDDKGILRQITLNDLPGVRSVDETLRVQAFQYTDKHEV	247	OX	NBCL_TaxID=6526;
Qy	245	CPAGWKPGSEETIPDPAGKLYFDKLN	271	RN	[1]
Db	248	CPAGWKPGSEETIPDPAGKLYFDKLN	274	RP	SEQUENCE FROM N. A.
RESULT 2					
O9Z0V5		PRELIMINARY;		RA	STRAIN=LAC; TISSUE=ALBUMEN GLAND;
ID	O9Z0V5	PRT;	273 AA.	RA	Cousin C., Ofori K., Okulate M., Grant J., Richards C., Lewis F.,
AC	9Z0V5;			RA	Knight M.;
DT	01-MAY-1999	(TREMBREL. 10, Created)		RT	"Biomphalaria glabrata: Molecular differences between the albumen
DT	01-MAY-1999	(TREMBREL. 10, Last sequence update)		RT	glands of susceptible and non-susceptible snails";
DT	01-JUN-2001	(TREMBREL. 17, Last annotation update)		RT	Submitted (JAN 2001) to the EMBL/GenBank/DDJB databases.
DE	PRX IV.			DR	EMBL; AY026256; AAK62361; -.
GN	PRX IV.			DR	HSPP; P30041; PRX.
OS	Rattus norvegicus (Rat).			DR	IntePro; IPR00866; Ahpc-TSA.
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			KW	Pfam; PRO0578; Ahpc-TSA; 1.
OX	NCBI_TaxID=10116;			FT	Peroxidase.
RN	[1]			SQ	SEQUENCE 223 AA; 1 1 25033 MW; B5B995442C1BF906 CRC64;
RP	SEQUENCE FROM N.A.			Query Match	60.9%; Score 877; DB 5; Length 223;
RX	MEDLINE:99148608; PubMed=10025941;			Best Local Similarity	76.5%; Pred. No. 3.7e-76;
RA	Matsumoto A., Okado A., Fujii T., Fujii J., Egashira M., Nikawa N.,			Matches	163; Conservative 18; Mismatches 30; Indels 2; Gaps 1;
RT	Taniguchi N.; "Cloning of the peroxiredoxin gene family in rats and characterization of the fourth member." RSL Lett. 443: 246-250(1999).			Qy	55 AGQQVYPGERSRVSADHSIHLASKAKISKEPAPWEGTAGTAVIDGEFRELKLTIDYRGKYLFF 114
RT	DR EMBL; AP106945; Aad17993.1; -.			Db	5 AGGGVPOEKR-T-TIGHIQWQSAVISRAPDNGTAVIKGEFKDKISDFKCKYLFF 62
DR	HSSP; P30041; PRX.			Qy	115 FYPUDFTFWCPCETIAFGDRLEERSINTEVACSVSDQFTHLAWINTPRQGGPIRI 174
DR	InterPro; IPR00866; Ahpc-TSA.			Db	63 FYPLDFTFWCPCETIAFGDRLEERSINTEVACSVSDQFTHLAWINTPRQGGPIRI 174
DR	Pfam; PF00578; Ahpc-TSA; 1.			Qy	175 PLISDLTHQISKDYGVYLEDSGHTRLGLFTIDDKGILRQITLNDLPGVRSVDETLRVQ 234
DR	SEQUENCE 273 AA; 31007 MW; 09E614794F1DC6C2 CRC64;			Db	123 PLISDITHESKAYGVQLQDGHSLRGLFTIDPKGTLRQITMNDLPGVRSVDETLRVQ 182
Qy	6 LIAATTPDHGRHRLL-PPLLELPAGAVQGWEEERPRTRBEECHFYAGQVPGF 63			Qy	235 FQYTDKHEGVCPAGWKPGSEETIPDPKSKYF 215
Db	7 LDLDGTPSR-RWRKVLVLLPPLFLQTEALOGLESDDFRTRRENCHFYAGQVPGF 65			Db	183 FQYTDKHEGVCPAGWKPGSEETIPDPKSKYF 215
Qy	64 ASRVSYVDHSIHLASKAKISKEPAPWEGTAGTAVIDGEFRELKLTIDYRGKYLFF 123			Qy	183 FQYTDKHEGVCPAGWKPGSEETIPDPKSKYF 215
Db	66 VSRVSVADHLSHLASKAKISKEPAPWEGTAGTAVIDGEFRELKLTIDYRGKYLFF 125			Qy	183 FQYTDKHEGVCPAGWKPGSEETIPDPKSKYF 215
Qy	124 CPTEIIFAGDRLEERSINTEVACSVSDQFTHLAWINTPRQGGPIRIPLSLTHQ 183			Qy	183 FQYTDKHEGVCPAGWKPGSEETIPDPKSKYF 215
Db	126 CPTEIIFAGDRLEEFKSINTEVACSVSDQFTHLAWINTPRQGGPIRIPLSLNHQ 185			Qy	183 FQYTDKHEGVCPAGWKPGSEETIPDPKSKYF 215
Qy	184 ISKDYGYYLEDSGHTRLGLFTIDDKGILRQITLNDLPGVRSVDETLRVQAFQYTDKHE 243			Qy	183 FQYTDKHEGVCPAGWKPGSEETIPDPKSKYF 215
Db	186 ISKDYGYYLEDSGHTRLGLFTIDDKGILRQITLNDLPGVRSVDETLRVQAFQYTDKHE 245			Qy	183 FQYTDKHEGVCPAGWKPGSEETIPDPKSKYF 215
Qy	244 VCPAGWKPGSEETIPDPAGKLYFDKLN 271			Qy	183 FQYTDKHEGVCPAGWKPGSEETIPDPKSKYF 215
Db	246 VCPAGWKPGSEETIPDPAGKLYFDKLN 273			Qy	183 FQYTDKHEGVCPAGWKPGSEETIPDPKSKYF 215
RESULT 3					
QB916	PRELIMINARY;	PRT;	223 AA.	RC	SEQUENCE FROM N. A.
ID	QB916			RC	STRAIN=BERKELEY;
AC	QB916;			RC	MDLINE=2019605; PubMed=10731132;
DT	01-JUN-2001 (TREMBREL. 17, Created)			RC	Adams M.D., Holt R.A., Evans C.A., Gocayne J.D.,
DT	01-JUN-2001 (TREMBREL. 17, Last sequence update)			RC	Leeds S.E., Holt R.A., Gallo R.F., Henderson S.N.,
DT	01-JUN-2002 (TREMBREL. 21, Last annotation update)			RC	Amanarides P.G., Scherer S.E., Li P.W., Hoskins R.A., Sutton G.G., Wostman J.R., Yandell M.D., Zhang Q., Chen L.X.,
DE	Thioredoxin peroxidase Bgtpx (fragment).			RC	George R.A., Levin S.E., Richard S., Ashburner M., Henderson S.N., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Nelson C.R., Miklos G.L.G.,
OS	Biomphalaria glabrata (Bloodlike planorb).			RC	Abrial J.F., Doyle C., Baxter E.G., Heit G., Nelson C.R., Baldwin D., Balley R.M., Bassu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beezon K.Y., Benos P.V., Brandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cowley S., Dahake C., Davenport L.B., Davies P., de Pablo J., Delcher A., Deng Z., May S., Dew I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Posler C., Gabrieleian A.B., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeawam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.C., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Mozny D.M., Nelson D.R.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pollard J., Puri V., Reese M.G.,
 RA Relmert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Staden-Klamos T., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrljgas R., Tector C., Turner R., Venner E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodward T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Ruben G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 SEQUENCE FROM N.A.
 RP MEDLINE=20098324; PubMed=10632718;
 RX Rodriguez J., Agudo M., van Damme J., Vandekerckhove J.,
 RA Santaren J.F.,
 RT "Polypeptides differentially expressed in imaginal discs define the
 peroxiredoxin family of genes in *drosophila*";
 RL Eur. J. Biochem. 267:487-497(2000).
 RN [3]
 SEQUENCE FROM N.A.
 RA Radyska S.N., Spinola B., Klichko V.I., Orr W.C.;
 RT "Cloning, expression and characterization of the peroxiredoxin gene
 submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 SEQUENCE FROM N.A.
 RP STRAIN=BERKELEY;
 RC Stapleton M., Brokstein P., Hong L., Aspaziani A., Carlson J.,
 RA Champé M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA González M., Guarín H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacieb J., Paragas V., Park S., Phoumanenavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Ceznik S.,
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AE033476; AAF47704.1; -;
 DR EMBL: AF42986.1; -;
 DR EMBL: AF221614; AAX06759.1; -;
 DR EMBL: AY000785; AAL28333.1; -;
 DR FBgn0040308; Jefrac2.
 DR InterPro: IPR000866; Abpc-TSA.
 DR Pfam: PF000578; Abpc-TSA; 1.
 KW Peroxidase.
 SQ SEQUENCE 242 AA; 26743 MW; 8A014FB191D9564 CRC64;
 Query Match 59.3%; Score 854.5; DB 5; Length 242;
 Best Local Similarity 65.2%; Pred. No. 6.1e-74;
 Matches 161; Conservative 29; Mismatches 48; Indels 9; Gaps 2;
 Qy 25 LLFLFLPAGAVQWGMETEERPTTREBECHEVAGQQVYPGEBSRVSVDHSIHLRSKAKISP
 ID 6 KAHVGKPAPEFOATAVNDGAFKEVKLSDYKGKVYLFFYPLDFTRVCPTEIVAFSDRAAE
 AC 78 KAKISKPKAPWPWEGTAVIDGEKFKELKLTDFRGKLYVFFFPLDFTRVCPPEIIFGDRLL
 Db 138 FRSLINTEVACSVDSOFTLIAWINTPRQRGGPRTPLISDLHQISDKYGVVLEDSGH
 Qy 198 TLRGLFTIDDKGKLRLQITLNDLPVGRSVDENLRLVQAFQYTDKIGEVCPAGWKPGSETII
 ID 6 FHKLNCELVGSVSDSOFTLIAWINTPRQRGGPRTPLISDLHQISDKYGVVLEDSGH
 Db 126 AYRGLEFVIDGKGVLQVQVITINDLPVGRSVDENLRLVQAFQYTDKIGEVCPAGWKPGSETII
 Qy 258 PDPACKLVYFDKLN 271
 ID 186 PNVDDSKKEYFSKHN 199
 SQ RESULT 6
 ID 09Y082
 AC 09Y082
 PRELIMINARY;
 PRY; 199 AA.
 DT 01-NOV-1999 (TREMBrel. 12, last sequence update)
 DT 01-MAR-2002 (TREMBrel. 20, last annotation update)
 DE Peroxiredoxin.
 GN TPX-1.
 OS Globodera rostochiensis (Golden nematode).
 OC Eukaryota; Metazoa; Nemataoda; Chromadorea; Tylenchina;
 OC Tylenchoidea; Heteroderidae; Heteroderinae; Globodera;
 OC NCBI_TaxID=31243;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=ROL;
 RX MEDLINE=20542028; PubMed=11087915;
 RA Robertson L., Robertson W.M., Sobczak M., Helder J., Tetaud E.,

Db 176 || :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||:||:||:||:
 Qy 265 KYFDKLN 271
 Db 236 KYFKANN 242
 RESULT 5
 ID 09BG13
 AC 09BG13;
 PRELIMINARY;
 PRY; 199 AA.
 DT 01-JUN-2001 (TREMBrel. 17, Last created)
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DE Peroxiredoxin 2.
 OS Bos taurus (Bovine).
 DR Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DR Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 DR Bovidae; Bovinae; Bos.
 DR NCBI_TaxID=9913;
 RN [1]
 SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Leyens G., Donnay I., Knops B.;
 RT "Cloning of 4 new bovine peroxiredoxins, and screening of the complete
 peroxiredoxin family in different bovine tissues";
 RT Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF05562; AAC53659.1; -;
 DR HSSP: P30041; 1PRX.
 DR InterPro: IPR000866; Abpc-TSA.
 DR Pfam: PF000578; Abpc-TSA; 1.
 SQ SEQUENCE 199 AA; 21946 MW; 5F256CE54090E2DE CRC64;
 Query Match 52.0%; Score 749; DB 6; Length 199;
 Best Local Similarity 69.1%; Pred. No. 5.4e-64;
 Matches 134; Conservative 26; Mismatches 34; Indels 0; Gaps 0;
 DR Sequence 199 AA.

RA	Ariyanayagan M.R.; Ferguson M.A.J.; Fairlamb A.; Jones J.T.;
RT	"Cloning, expression and functional characterisation of a peroxiredoxin from the potato cyst nematode <i>Globodera rostochiensis</i> ."; Mol. Biochem. Parasitol. 111:41-49 (2000).
RL	DR
EMBL	AJ243736; CAB48391.1;
HSSP	P30041; PRX5.
DR	InterPro; IPR00086; AhpC-TSA.
DR	PF00578; AhpC-TSA; 1.
SO	SEQUENCE 199 AA; 22317 MW; 90AD827467B0F53 CRC64;
Query Match	50.9%; Score 734; DB 5; Length 199;
Best Local Similarity	67.4%; Pred. No. 1.8e-62;
Matches	130; Conservative 30; Mismatches 33; Indels 0; Gaps 0;
Best Local Similarity	50.9%; Score 734; DB 5; Length 199;
Matches	130; Conservative 30; Mismatches 33; Indels 0; Gaps 0;
QY	77 SKAKISKPAPWEGTAVIDGEGEKFELKLTDYRGKLYVFFYPLDFPVCPTEIAFGDRLE 136
Db	5 SKAFICKPAPKFSDADEVNGEDEFTISLSDYKGKVWLFYPLDFTFCVCPTEIAFSRAD 64
QY	137 EFRSINTEVACVSUDSQFTHLAWINTPRROGGDRIPRLSLDTHQISKDYGYLESG 196
Db	65 EFKIDTQLIACSTDSKESHLIEWLNKPRKHGLEMKIPVLADPHNHSRBDYQHMEAG 124
QY	197 HTLRLGLIFIDDKGILRQITNDLPGVRSYDETDLRVLAQFOYTDKRGEVCPAGWPGSETI 256
Db	125 LAFRGFIDDDKGILRQITNDLPGVRSYDETDLRVLAQFOYTDKRGEVCPAGWPGSETI 184
QY	257 IPDPAGKLKYFDK 269
Db	185 KPDPEGSQTFFGK 197
RESULT 7	
09CW4	PRELIMINARY; PRT; 198 AA.
ID	09CW4; 01-JUN-2001 (Tremblrel. 17, Last sequence update)
AC	01-DEC-2001 (Tremblrel. 17, Last annotation update)
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE	Peroxiredoxin 2.
GN	
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TAXID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=<57BL6J>; TISSUE=EMBRYONIC STEM CELLS;
RX	MEDLINE=<2108560>; PubMed=<11217851;
RA	Kawai J., Shinagawa A., Shihata K., Yoshino M., Itch M., Ishii Y., Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Miyosawa H., Kondo S., Yamamoto T., Saito T., Okazaki Y., Gojobori T., Bonc H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batyalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pescce G., Quackenbush J., Scrimml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blaize J., Boitelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustincic S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombbert P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Suzuki H., Sato K., Schoenbach C., Seyta T., Storch K.-F., Wernshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y., Functional annotation of a full-length mouse cDNA collection. ";
RT	Nature 409:685-690(2001).; DR; EMBL; AK010653; BAB27093.1; -..; DR; HSSP; P30041; 1PRX2. MGD; MGI:109486; Prdx2. InterPro; IPR00086; AhpC-TSA. DR; Pfam; PF00578; AhpC-TSA; 1.
SO	SEQUENCE 198 AA; 21811 MW; 819FDD77A70259 CRC64;
Query Match	50.9%; Score 733; DB 11; Length 198;
Best Local Similarity	69.9%; Pred. No. 2.2e-62;
Matches	135; Conservative 23; Mismatches 35; Indels 0; Gaps 0;
QY	79 AKISKPAPWEGTAVIDGEGEKFELKLTDYRGKLYVFFYPLDFPVCPTEIAFGDRLEEF 138
Db	6 AQIGKSAPDFTATAVDGAFAKEIKLSDYRGKLYVFFYPLDFPVCPTEIAFSRAD 65
QY	139 RSINTEVACVSUDSQFTHLAWINTPRROGGDRIPRLSLDTHQISKDYGYLESGHT 198
Db	66 RKIGCEVLGVSYDSQFTHLAWINTPRKEGGGLSPNLLADITKSLSQNY3VNLNDIGIA 125
QY	199 LRGLFLIDDDKGILRQITNDLPGVRSYDETDLRVLAQFOYTDKRGEVCPAGWPGSETI 258
Db	126 YRGLFLIDDDKGILRQITNDLPGVRSVDEARLVLAQFOYTDKRGEVCPAGWPGSETI 185
QY	259 DPAGKLKYFDK 271
Db	186 NVDDSKEYFSRH 198
RESULT 8	
088376	PRELIMINARY; PRT; 198 AA.
ID	088376; 01-NOV-1998 (Tremblrel. 08, Created)
AC	01-Nov-1998 (Tremblrel. 08, Last sequence update)
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE	Type II peroxiredoxin 1.
GN	PRDX2 OR PRXII-1.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TAXID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=<129SVJ;
RX	MEDLINE=<9832838; PubMed=<9714804;
RA	Lim M.-J., Chae H.-Z., Rhee S.-G., Yu D.-Y., Lee K.-K., Yeom Y.I.; RT "The type II peroxiredoxin gene family of the mouse: molecular structure, expression and evolution."; Gene 216:197-205(1998);
DR	EMBL; AF032722; AAC35744.1; -
DR	EMBL; AF032718; AAC35744.1; JOINED.
DR	EMBL; AF032719; AAC35744.1; JOINED.
DR	EMBL; AF032720; AAC35744.1; JOINED.
DR	EMBL; AF032721; AAC35744.1; JOINED.
DR	HSSP; P30041; 1PRX.
DR	MGD; MGI:109486; Prdx2.
DR	InterPro; IPR00086; AhpC-TSA.
DR	Pfam; PF00578; AhpC-TSA; 1.
SO	SEQUENCE 198 AA; 21791 MW; EEFBF0F5426F7174D CRC64;
Query Match	50.5%; Score 727; DB 11; Length 198;
Best Local Similarity	69.4%; Pred. No. 8.3e-62;
Matches	134; Conservative 23; Mismatches 36; Indels 0; Gaps 0;
QY	79 AKISKPAPWEGTAVIDGEGEKFELKLTDYRGKLYVFFYPLDFPVCPTEIAFGDRLEEF 138
Db	6 AQIGKSAPDFTATAVDGAFAKEIKLSDYRGKLYVFFYPLDFPVCPTEIAFSRAD 65
QY	139 RSINTEVACVSUDSQFTHLAWINTPRROGGDRIPRLSLDTHQISKDYGYLESGHT 198
Db	66 RKIGCEVLGVSYDSQFTHLAWINTPRKEGGGLSPNLLADITKSLSQNY3VNLNDIGIA 125
QY	199 LRGLFLIDDDKGILRQITNDLPGVRSYDETDLRVLAQFOYTDKRGEVCPAGWPGSETI 258
Db	126 YRGLFLIDDDKGILRQITNDLPGVRSVDEARLVLAQFOYTDKRGEVCPAGWPGSETI 185
QY	259 DPAGKLKYFDK 271

RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seva T., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S., Hayashizaki Y.	QY	141 INTEVVACSVDSQFFTHLAWINTPRORGGLGPIRIPRLPSDLTHQISRDGYVYLEDGGHTLR 200
RA		Db	66 IGCSTIVGSIDSHFTHLAWINTPRQGGLBLRIPLLADKSMKISRDGYVLOEESCPFR 125
RA		Qy	201 GLFTIDDKGILRQITFLNDLVGRGSDTETLRLWQAQTYDTKHGEVNPAGWPGSETIIPD 260
RA		Db	126 GLFVTDQKQLRQTVNDLPVGRSVDETLRLVQAFQFTDEBGEVCPANWKPGSKTMADP 185
RA	"Functional annotation of a full-length mouse cDNA collection.";	Qy	261 AGKLYKFDKLN 271
RL	Nature 409:685-690(2001).		: : : :
DR	EMLBL: ARK005225; BAB23893.1; -.	Db	186 QKSKEFYNAAN 195
DR	HSSP; P30041; IPRX.		
DR	MGB; MG1:10486; Prdx2.		
DR	InterPro: IPR000866; Abpc-TSA.		
DR	Pfam; PF00578; Abpc-TSA; 1.		
SQ	SEQUENCE: 198 AA; 21847 MW; C378F57215EE4EE39 CRC64;		
	Search completed: January 17, 2003, 19:19:10		
	Job time : 42 secs		

	Query Match	Best Local Similarity	Score	DB	Length	11;
	Best Local Similarity	68.9%	Pred.	No.	6.1e-61;	Mismatches
Matches	133;	Conservative	22;	Mismatches	38;	Indels
QY	AKISKPAPWEGTAVIDGKELKLTDYRGKLVFFYPLDFTFCVCPTEIAFGDRLEEF	49.8%	Score	718;	DB	11;
QY	: : : : : : :	68.9%	Pred.	No. 6.1e-61;	Length	198;
Db	RSINTEVVACSVDSQFTHLAWINTPRROGGLSPTRIPLSLDTHOISKDGYGVLEDGHT	49.8%	Score	718;	DB	11;
Db	: : : : : :	68.9%	Pred.	No. 6.1e-61;	Length	198;
QY	66 RKRCEVIGVSVSDQSQFTLAWINTPRKEGGLGPNLNPILADVTKSLSHNYGVLNDEGA	49.8%	Score	718;	DB	11;
QY	139 LRLGFLIDDKGILRQITNLDPGRSDETLRIVQAQTYDKHGEVCPAGWKPGSETIP	49.8%	Score	718;	DB	11;
Db	126 YRGLFIIDTASGVLYRQITNLDPVGSRVDEALRLVQAFQYTDHEGEVCPAGWKPGSETIP	49.8%	Score	718;	DB	11;
QY	199 LRLGFLIDDKGILRQITNLDPGRSDETLRIVQAQTYDKHGEVCPAGWKPGSETIP	49.8%	Score	718;	DB	11;
Db	259 DRAGKLKVDFKL 271	49.8%	Score	718;	DB	11;
Db	186 NUDDSKEYFSKH 198	49.8%	Score	718;	DB	11;
RESULT	15					
QWSEF6						
ID	QWSEF6	PRELIMINARY;	PRT;	196 AA.		
AC	QWSEF6;					
DT	01-MAR-2002 (TREMBREL. 20, Created)					
DT	01-MAR-2002 (TREMBREL. 20, Last sequence update)					
DT	01-JUN-2002 (TREMBREL. 21, Last annotation update)					
DE	2-CYS thioredoxin peroxidase.					
TPX						
GN						
OS	Aedes aegypti (Yellowfever mosquito).					
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;					
OC	Phrygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;					
OC	Aedes.					
OX	NCBI_TAXID:7159;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=BLACK-EYED LIVERPOOL;					
RA	Fang J., Li J.;					
RT	"Isolation and characterization of Aedes aegypti thioredoxin peroxidase that contains two conserved cysteines.";					
RT	Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.					
DR	EMBL: AF323181; AAL37754.1; -.					
DR	InterPro: IPR000666; APCC-TSA.					
DR	pfam: PF00578; APBC-TSA; 1.					
KW	peroxidase.					
SQ	SEQUENCE 196 AA; 21862 MW; 3FDA8716A1A0EB2A CRC64;					
Query Match	49.8%	Score	717;	DB	5;	Length 196;
Best Local Similarity	68.6%	Pred.	No. 7.5e-61;			
Matches	131;	Conservative	24;	Mismatches	36;	Indels 0;
QY	81 ISRAPAPWEGTAVIDGKELKLTDYRGKLVFFYPLDFTFCVCPTEIAFGDRLEERS	49.8%	Score	717;	DB	5;
QY	140 LOKPAPKGTEATVNGKAREKEIKEDYGGKLVFFYPLDFTFCVCPTEIAFGDRLEERS	49.8%	Score	717;	DB	5;
QY	6 6 LOKPAPKGTEATVNGKAREKEIKEDYGGKLVFFYPLDFTFCVCPTEIAFGDRLEERS	49.8%	Score	717;	DB	5;

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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:15:02 ; Search time 11 Seconds

Perfect score: US-09-911-346-2
Sequence: 1 MEALPLLAATPDHGRRL... GSETTIPDPAGKLKYFDKLN 271

Title: 1021.826 Million cell updates/sec

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1441	100.0	271	1 PDX4_HUMAN	Q13162 homo sapien
2	1296	89.9	274	1 PDX4_BOVIN	09bg12 bos taurus
3	1262.5	87.6	274	1 PDX4_MOUSE	008807 mus musculus
4	749	52.0	199	1 PDX2_BOVIN	Q9bg13 bos taurus
5	746	51.8	198	1 PDX2_HUMAN	P32119 homo sapien
6	744	51.6	198	1 PDX2_RAT	P35704 rattus norvegicus
7	735.5	51.0	199	1 PDX1_HUMAN	Q06830 homo sapien
8	732	50.8	198	1 PDX2_MOUSE	Q61171 mus musculus
9	731.5	50.8	200	1 TDX_CYNPY	Q90384 cynops pyrrhura
10	730.5	50.7	199	1 PDX1_RAT	Q63716 rattus norvegicus
11	721.5	50.1	199	1 PDX1_MOUSE	P35700 mus musculus
12	703	48.8	256	1 PDX3_HUMAN	P30048 homo sapien
13	691	48.0	257	1 PDX3_BOVIN	P35705 bos taurus
14	689	47.8	257	1 PDX3_MOUSE	P20108 mus musculus
15	667	46.3	199	1 TDX_BRUMA	Q17172 brugia malayi
16	660	45.8	200	1 TDX_ONCMB	Q91191 oncorthynchus kroyeri
17	639.5	44.4	226	1 TDX1_GAEL	Q21824 caenorhabditis elegans
18	631.5	43.8	199	1 TDX_TYBIR	Q26595 trypanosoma brucei
19	592.5	41.1	210	1 BASI_HORVU	Q96468 hordeum vulgare
20	589	40.9	196	1 TSA1_CANAL	Q9Y770 candida albicans
21	588.5	40.8	210	1 BASL_WHEAT	P80602 tritium aestivum
22	584	40.5	195	1 TSAL YEAST	P34760 saccharomyces cerevisiae
23	582.5	40.4	265	1 BASL_SPOLT	Q24364 spinacia olaracea
24	571	39.6	266	1 BASL_ARATH	Q96791 arabidopsis thaliana
25	570.5	39.6	200	1 T755_SIN3	Q55624 synochocystis sp
26	567	39.3	195	1 TSA2 YEAST	Q04120 saccharomyces cerevisiae
27	561	38.9	194	1 TDX_FASHE	P91883 fasciola hepatica
28	556.5	38.6	229	1 TDX1_BRUMA	P48822 brugia malayi
29	548	38.0	199	1 YC2_PORPU	P51272 porphyra purpurea
30	489	33.9	127	1 PDX2_PIG	P52552 sus scrofa
31	479.5	33.3	233	1 CR29_ENTHI	P19476 entamoeba histolytica
32	477	33.1	178	1 R20K_CLOPA	P23161 clostridium perfringens
33	404	28.0	198	1 TSAA_HELPY	EMBL: U25182; AAB95175; 1; -.

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ALIGNMENTS

34	403	28.0	198	1 TSAA_HELPY	P21762 helicobacter pylori
35	398.5	27.7	197	1 TSAA_BUCA1	P57279 buchnera apicalis
36	394.5	27.4	204	1 YC42_ODST	P49537 odontella sphaerica
37	341	23.7	222	1 TDXH_AQUAE	Q67024 aquifex aeolicus
38	332	23.0	186	1 AHPC_ECOLI	P26427 escherichia coli
39	327	22.7	186	1 AHPC_SALTY	P19479 salmonella typhimurium
40	318.5	22.1	215	1 TDXH_THEMEA	Q9wz14 thermotoga maritima
41	316.5	22.0	199	1 TDX2_THEAC	Q9h113 thermoplasmatales
42	310.5	21.5	217	1 TDXH_METJIA	Q58146 methanococcus jannaschii
43	308	21.4	215	1 TDXH_SOULSO	P95895 sulfuribacillus soli
44	302	21.0	187	1 AHPC_BACSU	P80339 bacillus subtilis
45	291.5	20.2	215	1 TDXH_ARCFU	Q29569 archaeoglobus fumiferans

RESULT 1

PDX4_HUMAN

ID PDX4_HUMAN STANDARD PRT: 271 AA.

AC Q13162;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Peroxiredoxin 4 (EC 1.11.1.-) (Peroxidoxin 4 (EC 1.11.1.-)) (Thioredoxin peroxidase A0372)

DE (Thioredoxin-dependent peroxide reductase A0372) (Antioxidant enzyme AOE372) (AOE372-2).

PRDX4.

GN

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominoidea; Homo.

OX NCBI_TaxID=9606;

RP

RX

J. D.-Y., Choi, H.Z., Rhie, S.G., Jeang, K.-T.; "Regulatory role for a novel human thioredoxin peroxidase in NF-kappaB activation"; J. Biol. Chem. 272:30952-30961(1997).

RN [2]

SEQUENCE FROM N.A.

RA STRAUSBERG, R.

RA Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

RA TISSUE=Brain;

RA Strainsberg, R.;

RA Strainsberg, R.;

RA Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

RA OVEROXIDATION OF CYS-124.

RA Rabilloud, T.;

RA Unpublished observations (JUL-2002).

RA FUNCTION: Probably involved in redox regulation of the cell.

RA Regulates the activation of NF-kappa-B in the cytosol by a modulation of I-kappa-B-alpha phosphorylation.

RA SUBUNIT: Homodimer or heterodimer with PRDX1; disulfide-linked, upon oxidation (By similarity).

RA SUBCELLULAR LOCATION: Cytoplasmic.

RA -!- MISCELLANEOUS: The active site is the redox-active Cys-124 (to CYS-SOH) upon oxidative stress.

RA -!- SIMILARITY: BELONGS TO THE AHPC-TSA FAMILY.

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DR EMBL: BC007107; AAH07107.1; -.
 DR EMBL: BC016770; AAH16770.1; -.
 DR HSPP; P30041; IPRX.
 DR Genew; HGNC-17169; PRDX4.
 DR MIM; 606506; -.
 DR InterPro; IPR000866; AhPC-TSA.
 DR Pfam; PF00578; AhPC-TSA; 1.
 KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.
 FT DOMAIN; 20 30
 ACT SITE 124 124 REDOX-ACTIVE.
 FT DISULFID 124 245 INTERCHAIN (PARTIAL) (BY SIMILARITY).
 FT SEQUENCE 271 AA; 30540 MW; TE56B8004FC60F CRC64;
 SQ EMBL; AF30553; AAG53660.1; -.

Query Match 100.0%; Score 1441; DB 1; Length 271;
 Best Local Similarity 100.0%; Pred. No. 4.7e-126; Gaps 0;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEAPLLPLAATTDPDHGRRLRLLLPLFLPAGAVQGMETEERPRTREECHFYAGQQVY 60

Db 1 MEAPLLPLAATTDPDHGRRLRLLLPLFLPAGAVQGMETEERPRTREECHFYAGQQVY 60

QY 61 PGESARYSVADHSLHSKAKISKPKAPWEGTAVIDGSKELKLTDYRGKVLYFFYLDL 120

Db 61 PGESARYSVADHSLHSKAKISKPKAPWEGTAVIDGSKELKLTDYRGKVLYFFYLDL 120

QY 121 TFWCPTTEIAGDRLEERSINTEVAVACSVDSQFTHLAWINTPRQOGGLPIRPLSDL 180

Db 121 TFWCPTTEIAGDRLEERSINTEVAVACSVDSQFTHLAWINTPRQOGGLPIRPLSDL 180

QY 181 THQISKDGYVILEDSGHTLRGLFIDDKGILRQITNDLPGVRSVDETLRLVQAFOYTDK 240

Db 181 THQISKDGYVILEDSGHTLRGLFIDDKGILRQITNDLPGVRSVDETLRLVQAFOYTDK 240

QY 241 HGEVCPAGWKPOSESETIIPDPACKLKYFDKLN 271

Db 241 HGEVCPAGWKPOSESETIIPDPACKLKYFDKLN 271

RESULT 2

PDX4_BOVIN ID PDX4_BOVIN STANDARD; PRT; 274 AA.
 AC Q9BG12; ID PDX4_BOVIN STANDARD; PRT; 274 AA.
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Peroxiredoxin 4 (EC 1.11.1.-) (Prx-IV).

OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN [1] NEBL_TAXID=9913;
 RP SEQUENCE FROM N.A.
 RC TISSUE=liver;
 RL Levens G., Donnay I., Knoops B.;
 RT "Cloning of 4 new bovine-peroxiredoxins, and screening of the complete
 peroxiredoxin family in different bovine tissues.",
 Submitted (SEP-2000) to the EMBOGENbank/DBJ databases.

-!- FUNCTION: Probably involved in redox regulation of the cell.
 -!- Regulates the activation of NF-kappa-B in the cytosol by a
 modulation of I-kappa-B-alpha phosphorylation (By similarity).
 -!- SUBUNIT: Homodimer or heterodimer with PRDX1; disulfide-linked,
 upon oxidation (By similarity).
 -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 -!- MISCELLANEOUS: The active site is the redox-active Cys-127
 oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-248-SH of the
 other subunit to form an intermolecular disulfide with a
 concomitant homodimer formation. The enzyme may be subsequently
 regenerated by reduction of the disulfide by thioredoxin (By
 similarity).
 -!- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-
 127 (to Cys-503H) upon oxidative stress (By similarity).

CC -!- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
 CC -----
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 or send an email to licenses@isb-sib.ch).-----
 CC -----
 DR EMBL; AF30553; AAG53660.1; -.

DR InterPro; IPR000866; AhPC-TSA.
 DR Pfam; PF00578; AhPC-TSA; 1.
 KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.
 FT ACT SITE 127 248 INTERCHAIN (PARTIAL) (BY SIMILARITY).
 FT DISULFID 127 248 INTERCHAIN (PARTIAL) (BY SIMILARITY).
 SQ EMBL; AF30553; AAG53660.1; -.

Query Match 89.9%; Score 1296; DB 1; Length 274;
 Best Local Similarity 92.1%; Pred. No. 1.3e-112; Gaps 0;
 Matches 246; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 5 PLAAATTDPDHGRRLRLLLPLFLPAGAVQGMETEERPRTREECHFYAGQQVPGEA 64

Db 8 PPUPATLAPGRSRKLLLPLFLPAGAVQGMETEERPRTREECHFYAGQQVPGEA 67

QY 65 SRVSYVAHSLSKAKISKPKAPWEGTAVIDGSKELKLTDYRGKVLYFFYPLDFEV 124

Db 68 SRVSYVAHSLSKAKISKPKAPWEGTAVIDGSKELKLTDYRGKVLYFFYPLDFEV 127

QY 125 PTIIEAGDRLEERSINTEVAVACSVDSQFTHLAWINTPRQOGGLSINIPILLADNHQI 184

Db 128 PTIIEAGDRLEERSINTEVAVACSVDSQFTHLAWINTPRQOGGLSINIPILLADNHQI 187

QY 185 SKDGYVILEDSGHTLRGLFIDDKGILRQITNDLPGVRSVDETLRLVQAFOYTDKIGEV 244

Db 188 SKDGYVILEDSGHTLRGLFIDDKGILRQITNDLPGVRSVDETLRLVQAFOYTDKIGEV 247

QY 245 CRPGWKPOSESETIIPDPACKLKYFDKLN 271

Db 248 CPAGWKPOSESETIIPDPACKLKYFDKLN 274

RESULT 3

PDX4_MOUSE ID PDX4_MOUSE STANDARD; PRT; 274 AA.
 AC O08807; ID PDX4_MOUSE STANDARD; PRT; 274 AA.
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Peroxiredoxin 4 (EC 1.11.1.-) (Prx-IV) (Thioredoxin peroxidase A0372)
 DE (thioredoxin-dependent peroxide reductase A0372).
 DE A0372).

GN PRDX4.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RL NCBI_TaxID=10090;
 RN [1] SEQUENCE FROM N.A.

RP STRAIN=IC57BL/6J;
 RX MEDLINE=2121079; Pubmed=11229364;
 RA Wong C.M., Chun A.C., Kok K.H., Zhou Y., Fung P.C., Kung H.F.,
 RA Jeang K.-T., Jin D.-Y.;
 RT Characterization of human and mouse peroxiredoxin IV: evidence for
 inhibition by PRX-IV of epidermal growth factor- and p53-induced
 reactive oxygen species.
 RL Antioxid. Redox. Signal. 2;507-518(2000).
 -!- FUNCTION: Probably involved in redox regulation of the cell.
 CC Regulates the activation of NF-kappa-B in the cytosol by a
 modulation of I-kappa-B-alpha phosphorylation.
 CC -!- SUBUNIT: Homodimer or heterodimer with PRDX1; disulfide-linked,

CC upon oxidation.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- MISCELLANOUS: The active site is the redox-active Cys-127 oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-248-SH of the other subunit to form an intermolecular disulfide with a concomitant homodimer formation. The enzyme may be subsequently regenerated by reduction of the disulfide by thioredoxin (By similarity).

CC -!- MISCELLANOUS: Irreversibly inactivated by overoxidation of Cys-127 (to Cys-SO3H) upon oxidative stress (By similarity).

CC -!- SIMILARITY: BELONGS TO THE AHC/TSA FAMILY.

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RA Leyens G.; Donay I.; Knops B.;

RT "Cloning of 4 new bovine peroxiredoxins, and screening of the complete peroxiredoxin family in different bovine tissues";

RT Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: Involved in redox regulation of the cell. Reduces peroxides with reducing equivalents provided through the thioredoxin system. It is not able to receive electrons from glutaredoxin. May play an important role in eliminating peroxides generated during metabolism. Might participate in the signaling cascades of growth factors and tumor necrosis factor-alpha by regulating the intracellular concentrations of H2O2(2).

CC -!- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- MISCELLANOUS: The active site is the redox-active Cys-52 oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-173-SH of the other subunit to form an intermolecular disulfide with a concomitant homodimer formation. The enzyme may be subsequently regenerated by reduction of the disulfide by thioredoxin (By similarity).

CC -!- MISCELLANOUS: Irreversibly inactivated by overoxidation of Cys-52 (to Cys-SO3H) upon oxidative stress (By similarity).

CC -!- SIMILARITY: BELONGS TO THE AHC/TSA FAMILY.

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DR Pfam; PF00578; Ahpc-TSA; 1.

DR HSSP; P30041; 1PRX

DR PMMA; 2DPAGE; 008807; -.

DR MGI; MGI-1859815; Prdx4.

DR DRINTERPRO; IPK00866; Ahpc-TSA.

DR Pfan; PR00578; Ahpc-TSA; 1.

DR KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center.

FT ACT_SITE 127 17 REDOX-ACTIVE (BY SIMILARITY).

FT DISULFID 127 248 INTERCHAIN (PARTIAL) (BY SIMILARITY).

SEQUENCE 274 AA; 31052 MW; 73DB5374EC46241C CRC64;

Query Match 87.6%; Score 1262.5; DB 1; Length 274;

BEST Local Similarity 89.1%; Pred. No. 5e-109; Mismatches 10; Indels 3; Gaps 2;

Matches 244; Conservative 10; Mismatches 17; Indels 3; Gaps 2;

Qy 1 MEA-LPLLAATTDPHGRHRRLLL--PLFLFLPAGAVOGWEEPERPREEECHFYAGG 57

1 MEARKSKLDGTTASRRWRTRKLVLILLPLPLFLIRTELESQGLSDERFRTRRENCHFYAGG 60

Db QYVPGGEASRVSDVADSLHLHKSAKISKPKAPYWESEPAVIGEKFELKLTITYRGKLVFFYP 117

61 QVYGEASRVSDVADSLHLHKSAKISKPKAPYWESEPAVINGEKFELKLTITYRGKLVFFYP 120

Qy 118 LDEFFVFCPEIIFAGDRLEFRSINTEVAVACSDSOFTHLAWNTPRROGGGLPPIPL 177

121 LDFIFVCPTEIIFAGDRLEFKINTEVAVACSDSOFTHLAWNTPRROGGGLPPIPL 180

Qy 178 SDLTHQISKDGYVYLEDSGHTLRGLFLIFTDDKGILRQITNDLPVGRSYDETLRUVQATQY 237

181 SDLNHQISKDGYVYLEDSGHTLRGLFLIFTDDKGILRQITNDLPVGRSYDETLRUVQATQY 240

Qy 238 TDHGEGEPAGWPGSETIIPDAGKLKYFDKLN 271

Db 241 TDKGEGVCAGWKQGETIIPDAGKLKYFDKLN 274

RESULT 4

PDX2_BOVIN STANDARD; PRT; 199 AA.

ID PDX2_BOVIN

AC Q9BQ13;

DT 15-JUN-2002 (Rel. 41, last sequence update)

DT 15-JUN-2002 (Rel. 41, last annotation update)

DE Peroxiredoxin 2 (EC 1.11.1.-).

GN PDX2.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

[1] SEQUENCE FROM N.A.

RP TISSUE=Liver;

RC

RESULT 5

PDX2_HUMAN STANDARD; PRT; 198 AA.

ID PDX2_HUMAN

AC P35701; P31945; Q92763;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-NOV-1997 (Rel. 35, last sequence update)

DT 15-JUN-2002 (Rel. 41, last annotation update)

DE Peroxiredoxin 2 (EC 1.11.1.-) (Thioredoxin-dependent peroxidase/reductase 1) (Thiol-specific antioxidant protein) (TSAP) (PRPF) (Natural killer cell enhancing factor B) (NKEF-B).

DE PRDX2 OR TDPX1 OR NKEFB.

GN Homo sapiens (Human).

AC PDX1-MOUSE STANDARD; PRT; 199 AA.
 DR EMBL: ABC03563; BAA86992.1; JOINED.
 DR P35700; PIR: A48533; A48513.
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DR PIR: JC2259; JC2259.
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DR HSSP; P30041; IPRX.
 DE peroxiredoxin 1 (EC 1.11.1.-) (Thioredoxin-dependent peroxide reductase 2) (Osteoblast specific factor 3) (OSF-3) (Macrophage 23 kDa stress protein).
 DE PRDX1 OR TDX1 OR MSP23 OR PAGA.
 OS MUS; musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=1090;
 RN [1] SEQUENCE FROM N.A.
 RC TISSUE=Peritoneal macrophage;
 RX MEDLINE=9336671; Pubmed=8360158;
 RA Ishii T., Yamada M., Sato H., Matsue M., Taketani S., Nakayama K., Sugita Y., Banai S.;
 RT Cloning and characterization of a 23-kDa stress-induced mouse peritoneal macrophage protein.;
 J. Biol. Chem. 268:18633-18636(1993).
 RN [2] SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=osteoblast;
 RX MEDLINE=9435405; Pubmed=8089076;
 RA Kawai S., Takeshita S., Okazaki M., Kikuno R., Kudo A., Amann E.;
 RT "Cloning and characterization of OSF-3, a new member of the MERS family, expressed in mouse osteoblastic cells.";
 RL J. Biochem. 115:641-643(1994).
 RN [3] SEQUENCE FROM N.A.
 RC STRAIN=129/SVJ; TISSUE=Liver;
 RA Hino K., Sato H., Banai S.;
 RT Characterization of mouse type I peroxiredoxin gene and pseudogenes.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 CC -I- FUNCTION: Involved in redox regulation of the cell. Reduces peroxides with reducing equivalents provided through the thioredoxin system but not from glutaredoxin. May play an important role in eliminating peroxides generated during metabolism. Might participate in the signaling cascades of growth factors and tumor necrosis factor-alpha by regulating the intracellular concentrations of H(2)O(2).
 CC -I- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By similarity). May form heterodimers with AOP2.
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -I- TISSUE SPECIFICITY: FOUND IN VARIOUS TISSUES; HIGH CONCENTRATION IN LIVER.
 CC -I- INDUCTION: BY OXIDATIVE AND SULFYDRYL-REACTIVE AGENTS.
 CC -I- MISCELLANEOUS: The active site is the redox-active Cys-52 oxidized to CYS-SOH. Cys-SOH rapidly reacts with Cys-173-SH of the other subunit to form an intermolecular disulfide with a concomitant homodimer formation. The enzyme may be subsequently regenerated by reduction of the disulfide by thioredoxin (By similarity).
 CC -I- MISCELLANEOUS: Irreversibly inactivated by overoxidation of Cys-52 (to CYS-SO3H) upon oxidative stress (By similarity).
 CC -I- SIMILARITY: BELONGS TO THE AOP/C/TSA FAMILY.
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RN [1] SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=95251598; Pubmed=7733872;
 RA Tsujii K., Copeland N.G., Jenkins N.A., Obinata M.;
 RT Mammalian antioxidant protein complements alkylhydroperoxide reductase (ahpc) mutation in Escherichia coli.;
 RL Biochem. J. 307:377-381(1995).
 RN [2] SEQUENCE FROM N.A.
 RC TISSUE=Spleen, Testis, Urinary bladder, and Uterus;
 RA Strauberg R.;
 RT Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 RN [3] SEQUENCE OF 148-240 FROM N.A.
 RX MEDLINE=94108427; Pubmed=7506601;
 RA Takeda J., Yano H., Eng S., Zeng Y., Bell G.I.;
 RA RT "A molecular inventory of human pancreatic islets: sequence analysis of 1000 cDNA clones.";
 RL Hum. Mol. Genet. 2:1793-1798(1993).
 RN [4] SEQUENCE OF 63-72.
 RC TISSUE=Liver;
 RX MEDLINE=93162045; Pubmed=1286669;

		RESULT 13
PDX3-BOVIN	ID PDX3-BOVIN	STANDARD; PRT; 257 AA.
AC P35705;	DT 01-JUN-1994 (Rel. 29, Created)	DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC	DT 15-JUN-2002 (Rel. 41, Last annotation update)	DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC	DE Thioredoxin-dependent peroxide reductase, mitochondrial precursor (EC 1.11.1.-) (Peroxiredoxin 3) (Antioxidant protein 1) (ROP-1) (SP-22) protein	DE Thioredoxin-dependent peroxide reductase, mitochondrial precursor (EC 1.11.1.-) (Peroxiredoxin 3) (Antioxidant protein 1) (ROP-1) (SP-22) protein
CC	PRDX3 OR ROP1.	PRDX3 OR ROP1.
CC	OS Bos taurus (Bovine)	OS Bos taurus (Bovine)
CC	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;	CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
CC	OC Bovidae; Bovinae; Bos.	OC Bovidae; Bovinae; Bos.
CC	OX NCBI-TAXID=9913;	OX NCBI-TAXID=9913;
CC	RN [1] SEQUENCE FROM N.A.	RN [1] SEQUENCE FROM N.A.
CC	RC TISSUE=Adrenal medulla;	RC TISSUE=Adrenal medulla;
CC	RX MEDLINE=97069947; PUBMED=8912927;	RX MEDLINE=97069947; PUBMED=8912927;
CC	RA Hiroi T., Watabe S., Takimoto K., Yago N., Yamamoto Y., Takahashi S.Y.;	RA Hiroi T., Watabe S., Takimoto K., Yago N., Yamamoto Y., Takahashi S.Y.;
CC	CC "The cDNA sequence encoding bovine SP-22, a new defence system against reactive oxygen species in mitochondria.",	CC "The cDNA sequence encoding bovine SP-22, a new defence system against reactive oxygen species in mitochondria.",
CC	RL DNA Seq. 6:239-242(1996).	RL DNA Seq. 6:239-242(1996).
CC	RN [2] SEQUENCE OF 2-257 FROM N.A.	RN [2] SEQUENCE OF 2-257 FROM N.A.
CC	RC TISSUE=adrenal medulla;	RC TISSUE=adrenal medulla;
CC	RX MEDLINE=94137540; PUBMED=8089078;	RX MEDLINE=94137540; PUBMED=8089078;
CC	RA Watabe S., Kohno H., Kouyama H., Hiroi T., Yago N., Nakazawa T.;	RA Watabe S., Kohno H., Kouyama H., Hiroi T., Yago N., Nakazawa T.;
CC	CC "Purification and characterization of a substrate protein for mitochondrial Atp-dependent protease in bovine adrenal cortex.",	CC "Purification and characterization of a substrate protein for mitochondrial Atp-dependent protease in bovine adrenal cortex.",
CC	RL J. Biochem. 115:648-654(1994).	RL J. Biochem. 115:648-654(1994).
CC	CC -!- FUNCTION: Involved in redox regulation of the cell. Protects radical-sensitive enzymes from oxidative damage by a radical-	CC -!- FUNCTION: Involved in redox regulation of the cell. Protects radical-sensitive enzymes from oxidative damage by a radical-
CC	CC generating system.	CC generating system.
CC	CC -!- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By similarity).	CC -!- SUBUNIT: Homodimer; disulfide-linked, upon oxidation (By similarity).
CC	CC -!- SUBCELLULAR LOCATION: Mitochondrial.	CC -!- SUBCELLULAR LOCATION: Mitochondrial.
CC	CC -!- MISCELLANEOUS: The active site is the redox-active Cys-109 oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-230-SH of the other subunit to form an intermolecular disulfide with a concomitant homodimer formation. The enzyme may be subsequently regenerated by reduction of the disulfide (By similarity).	CC -!- MISCELLANEOUS: The active site is the redox-active Cys-109 oxidized to Cys-SOH. Cys-SOH rapidly reacts with Cys-230-SH of the other subunit to form an intermolecular disulfide with a concomitant homodimer formation. The enzyme may be subsequently regenerated by reduction of the disulfide (By similarity).
CC	CC -!- SIMILARITY: BEONGS TO THE AHPCT/ASA FAMILY.	CC -!- SIMILARITY: BEONGS TO THE AHPCT/ASA FAMILY.
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	DR EMBL; D82025; BRAI1511.1; -.	DR EMBL; D82025; BRAI1511.1; -.
CC	DR InterPro; IPR000866; Ahpc-TSA.	DR InterPro; IPR000866; Ahpc-TSA.
CC	DR Pfam; PF00578; Ahpc-TSA; 1.	DR Pfam; PF00578; Ahpc-TSA; 1.
CC	KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center;	KW Antioxidant; Peroxidase; Oxidoreductase; Redox-active center;
CC	KW MITOCHONDRIAL; TRANSIT PEPTIDE.	KW MITOCHONDRIAL; TRANSIT PEPTIDE.
CC	FT TRANSIT 1 62 MITOCHONDRIUM.	FT TRANSIT 1 62 MITOCHONDRIUM.
CC	FT CHAIN 63 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.	FT CHAIN 63 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.
CC	FT ACT_SITE 108 REDOX ACTIVE (BY SIMILARITY).	FT ACT_SITE 108 REDOX ACTIVE (BY SIMILARITY).
CC	FT DISULFID 108 229 INTERCHAIN (PARTIAL) (BY SIMILARITY).	FT DISULFID 108 229 INTERCHAIN (PARTIAL) (BY SIMILARITY).
CC	FT CONFLICT 31 R->W (IN REF. 2; AAO03435).	FT CONFLICT 31 R->W (IN REF. 2; AAO03435).
CC	SQ 256 AA; 27692 MW; 8BB7F5E55BFEE9BE CRC64;	SQ 256 AA; 27692 MW; 8BB7F5E55BFEE9BE CRC64;
CC	Query Match 48.8%; Score 703; DB 1; Length 256; Best Local Similarity 66.5%; Pred. No. 9.1e-58; Matches 127; Conservative 28; Mismatches 36; Indels 0; Gaps 0;	Query Match 48.8%; Score 703; DB 1; Length 256; Best Local Similarity 66.5%; Pred. No. 9.1e-58; Matches 127; Conservative 28; Mismatches 36; Indels 0; Gaps 0;
CC	OY 81 ISKPAPWEGTAGTAVIDGERKEELKLTDYRGKLVFFYPLDFTWCPTELIAFGDRLEEFFS 140	OY 81 ISKPAPWEGTAGTAVIDGERKEELKLTDYRGKLVFFYPLDFTWCPTELIAFGDRLEEFFS 140
CC	DB 65 VHQHAPYEWKGATGATVNGEKKFLSDUDFKKKYLVLFYPLDFTWCPTELIAFGDRLEEFFS 124	DB 65 VHQHAPYEWKGATGATVNGEKKFLSDUDFKKKYLVLFYPLDFTWCPTELIAFGDRLEEFFS 124
CC	DB 141 INTEPVWAGSVSDSOPTHLAWINTPRQGGLGPIRPLSLDTHOISKDGYVYLEDSGHTR 200	DB 141 INTEPVWAGSVSDSOPTHLAWINTPRQGGLGPIRPLSLDTHOISKDGYVYLEDSGHTR 200
CC	DB 125 VNCCEVWAVSYVDSHFLAWINTPRKNGGLGHMNTALLSDLTKQISRDYGVLEGSGLAR 184	DB 125 VNCCEVWAVSYVDSHFLAWINTPRKNGGLGHMNTALLSDLTKQISRDYGVLEGSGLAR 184
CC	DB 201 GLFTIDDKGILRQLTLDLPGVGSVDETRLQAFQYDQKHEVCPAGWKPGSTIIPD 260	DB 201 GLFTIDDKGILRQLTLDLPGVGSVDETRLQAFQYDQKHEVCPAGWKPGSTIIPD 260
CC	DB 185 GLFTIDPVGKVHLVNSNDLPGRSVEETRLVKAFQYVETHGEVCPANWPDSPTIKPP 244	DB 185 GLFTIDPVGKVHLVNSNDLPGRSVEETRLVKAFQYVETHGEVCPANWPDSPTIKPP 244
CC	QY 261 AGKLYKFDKLN 271	QY 261 AGKLYKFDKLN 271

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or send an email to license@ibb-sib.ch.

EMBL; U47100; AAB67873.1; -.

InterPro; IPR000866; Ahpc-TSA.

pram; pF005/8; Ahpc-TSA; I.

ACT_SITE 53 BY SIMILARITY.
ACT_SITE 174 BY SIMILARITY.

SEQUENCE 199 AA; 22042 MW; 8932BD88898B271B CRC64;

every Match Score 667; DB 1; Length
est local similarity 63.7%; pred NC 1 1e-54.

Matches 123; Conservative 26; Mismatches 44; Inde-

77 SKAKISKPAPYWEGTAVIDGEFKEKLTxDYRGKYLVFFFYPLDFTFCVCP

6 SKAFIGQOPAPNFKTTAVVNGDFKETISLGQFKGKYVULLFYPLDFTFVCP

137 EFRSINTEVACSVPSOFTLAWINTPROGGLGPISRIPPLESBTHOISS

66 EFKOLDYAVVMACSTDHSFESHLAWNTDRKMGCGOMNTPTIAVTNHVTS

187 *HEMISFERIUM HISTORICO-ARTIFICIALE*

157 MURGE LUDRAGLQVNDLPGRSVDEILKLUQA QIDRGEVC
158 ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
159 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
160 :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :

126 IAYRGLFIIIDPKGILGQITINBLPVGRSVBETLRLIQAFQFVBKRIGEV

257 IPDPAGKLKYFDK 269

186 KPGVKESKAYFEK 198

CCW completed: January 17 2003 19:17:39

time : 17 secs

ເລກມີ 1 : ໂກງ ພຣ

ເລກມີ 1 : ໂກງ ພຣ

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